

	114124	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	24.2	242	10	5.6
	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	6.7	67	1	6.3
	114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.8	73	19	1.8
	114196	AF017445	Hs.150926	fucose-1-phosphata guanylyltransferase	4.4	104	24	5.1
5	114208	AL049466	Hs.7859	ESTs	5.7	57	1	4.9
	114239	AL137667	Hs.267445	Homo sapiens mRNA; cDNA DKFZp434B231 (fr	3.3	33	1	2.4
	114251	H15261	Hs.21948	ESTs	4.2	46	11	1.4
	114306	AF100143	Hs.6540	fibroblast growth factor 13	4.5	45	2	3
	114460	AF183810	Hs.26102	trichorhinophalangeal syndrome I	4.4	44	1	3
10	114542	AW970128	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	4.7	770	166	5.8
	114652	AI521936	Hs.107149	novel protein similar to archaeal, yeast	5.2	52	3	2.3
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	4.6	196	43	10
	114768	AF212848	Hs.182339	ets homologous factor	13.7	137	1	8.9
	114774	AV656017	Hs.184325	CGI-76 protein	3.3	168	51	7.3
15	114798	AA159181	Hs.54900	serologically defined colon cancer antig	7.4	137	19	1.8
	114821	AI648602	Hs.55468	ESTs	4.7	57	12	4.7
	114880	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.1	91	1	7.6
	114918	BE165762	Hs.23518	hypothetical protein from BCRA2 region	10.1	111	11	10.2
	114940	BE092696	Hs.75928	ESTs	6.4	67	11	5
20	114965	AI733881	Hs.72472	BMP-R1B	35.9	359	10	29.7
	114969	AW162998	Hs.24684	KIAA1376 protein	9.4	94	8	7.3
	114988	AA251089		gb:zs04f05.s1 NCLCGAP_GCB1 Homo sapiens	11.5	115	1	6.9
	115004	AA329340	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-	4.2	42	9	1.1
	115054	AW265668	Hs.87729	hypothetical protein FLJ12428	5.1	51	1	4.2
25	115061	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	4.6	290	65	3.7
	115140	NM_014158	Hs.279338	HSPC067 protein	4.8	48	1	4.4
	115142	AI623693	Hs.191533	ESTs	3.2	49	16	4.2
	115188	AK000219	Hs.88367	hypothetical protein FLJ20212	3.3	33	1	3
	115206	AW183695	Hs.186572	ESTs	5.8	58	1	5
30	115221	AW365434	Hs.79741	hypothetical protein FLJ10116	5.5	343	62	2.5
	115262	AI422867	Hs.88594	ESTs	11.2	112	1	10.3
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461	4.5	96	21	7.8
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	5.9	59	1	4.2
	115583	NM_012317	Hs.45231	leucine zipper, down-regulated in cancer	9.8	98	1	8.8
35	115600	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fls, clone NT	4.6	46	2	1.8
	115622	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	4.4	44	7	1.1
	115646	N36110	Hs.305971	solute carrier family 2 (facilitated glu	3.2	372	115	2.1
	115674	AW992358	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	10.2	506	50	2.8
	115675	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	5.2	405	78	10.1
40	115719	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	7.6	144	19	13.9
	115725	AW890653	Hs.76917	F-box only protein 8	3.1	58	19	2.5
	115764	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	5.7	368	65	28.5
	115821	AW338063	Hs.130965	zinc-finger protein ZBRK1	3.9	39	8	2.2
	115825	R50956	Hs.159993	glycosyltransferase	4.2	79	19	1.9
45	115839	BE300266	Hs.28935	transducin-like enhancer of split 1, hom	5.8	58	1	4.4
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	6.2	62	1	5.4
	115892	AA291377	Hs.50831	ESTs	3.2	40	13	0.7
	115967	AI745379	Hs.42911	ESTs	8.4	101	12	6.7
	116093	AW673312	Hs.50848	hypothetical protein FLJ20331	3.6	36	1	2
50	116097	AI198719	Hs.176376	ESTs	5.1	51	1	2
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	3.4	34	8	1
	116127	AF126743	Hs.279884	DNAJ domain-containing	3.5	35	8	3.3
	116129	AF189011	Hs.49163	putative ribonuclease III	4.5	45	9	3.4
	116204	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fls, clone PL	5.2	52	4	3.9
55	116226	AW976438	Hs.17428	RBP1-like protein	3.8	38	7	2.1
	116238	AV660717	Hs.47144	DKFZP586N0819 protein	5.1	198	39	17.9
	116250	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheri	13.3	133	8	3.2
	116256	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	3.3	106	33	9.8
	116298	AI955411	Hs.94109	Homo sapiens cDNA FLJ13634 fls, clone PL	4.8	179	38	2.8
60	116336	AL133033	Hs.4084	KIAA1025 protein	3.2	173	55	3
	116351	AL133623	Hs.82501	similar to mouse Xrn1 / Dhm2 protein	3.7	37	1	1.8
	116366	N50174	Hs.46765	ESTs	3.9	39	10	0.6
	116379	AA448588	Hs.71252	hypothetical protein DKFZp761C169	5.6	106	19	9
	116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.6	256	72	3.7
65	116450	AI654450	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.1	119	39	2
	116461	AA313607	Hs.58633	Homo sapiens cDNA: FLJ22145 fls, clone H	5.5	315	58	3.1
	116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.4	496	144	1.6

5	116507	AI418366	Hs.68501	ESTs	3.1	31	4	1.9
	116579	AW888411	Hs.81915	leukemia-associated phosphoprotein p18 (3.3	931	279	5.6
	116625	F01801	Hs.241567	RNA binding motif, single stranded Inter	3.6	36	1	1.9
	116674	AI768015	Hs.92127	ESTs	4.5	96	22	6.9
	116680	AW902848	Hs.273829	ESTs	4.2	42	1	2.7
10	116710	F10577	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	7.1	71	9	6.9
	116724	AA741307	Hs.65641	hypothetical protein FLJ20073	4.3	190	44	5.4
	116786	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	22.8	228	9	12.4
	116787	AW362955	Hs.15641	Homo sapiens cDNA FLJ14415 fis, clone HE	4.9	108	22	9
	116790	AW161357	Hs.101174	microtubule-associated protein tau	4.6	163	35	7.3
15	116844	H64938	Hs.337434	ESTs, Weakly similar to A46010 X-linked	6.9	69	10	2.4
	117027	AW085208	Hs.130093	ESTs	4.8	48	1	2.5
	117067	H91164	Hs.335797	ESTs	3.3	33	1	2.3
	117129	H95785	Hs.167652	ESTs, Highly similar to 1819485A CENP-E	3.1	38	13	1.7
	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	4.8	48	1	0.9
20	117170	N25929	Hs.42500	ADP-ribosylation factor-like 5	3.1	295	96	27.9
	117209	W03011	Hs.306881	MSTP043 protein	3.6	41	12	2.8
	117280	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C	3.9	322	83	4.4
	117367	AI041793	Hs.42502	ESTs	3.5	72	21	1.3
	117412	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	17.4	174	9	6.9
25	117475	N30205	Hs.93740	ESTs, Weakly similar to 138022 hypotheti	3.2	35	11	0.7
	117634	AW341639	Hs.13323	hypothetical protein FLJ22059	5	50	1	4.7
	117667	U59305	Hs.44708	Ser-Thr protein kinase related to the my	4.5	211	47	5
	117852	AW877787	Hs.136102	KIAA0853 protein	4.6	46	1	3.8
	117873	N48967	Hs.46624	HSPC043 protein	3.1	31	1	2.7
30	117924	AI521436	Hs.38891	ESTs	4.9	49	1	4.4
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	5	50	2	3.1
	118449	AI813865	Hs.164478	hypothetical protein FLJ21939 similar to	3.6	89	25	0.9
	118467	AF091434	Hs.43080	platelet derived growth factor C	3.2	378	117	2.8
	118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	14.5	145	1	2.4
35	118475	N86845	Hs.43228	gb:za46c11.s1 Soares fetal liver spleen	3.1	199	64	1
	118509	N22617	Hs.43228	Homo sapiens cDNA FLJ11835 fis, clone HE	6	60	5	3.7
	118528	AI949952	Hs.49397	ESTs	3.3	81	25	1.5
	118828	N79496	Hs.50824	EST, Moderately similar to 154374 gene N	3.4	740	217	2.8
	118836	AW134482	Hs.173001	hypothetical protein FLJ13964	4.3	162	38	12.1
40	118854	T58283	Hs.10450	Homo sapiens cDNA: FLJ22063 fis, clone H	3.4	118	35	2.3
	118873	AI824009	Hs.44577	ESTs	3.5	35	1	2.9
	118888	AI191811	Hs.54629	ESTs	8.4	84	10	0.8
	118901	AW292577	Hs.94445	ESTs	7.3	73	3	5.4
	118981	N29309	Hs.39288	ESTs	5	50	5	4.7
45	118991	NM_016657	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.7	37	6	0.5
	119023	N98488	Hs.90790	gb:zb82h01.s1 Soares_senescen_fibroblas	3.3	36	11	0.6
	119088	R39261	Hs.117183	Homo sapiens cDNA: FLJ22930 fis, clone K	3.3	167	51	2.6
	119126	R45175	Hs.92482	ESTs	5.3	53	6	2.3
	119128	H09334	Hs.65328	ESTs	3.7	37	4	3
50	119271	AI061118	Hs.155478	Fanconi anemia, complementation group F	8.2	82	1	6.4
	119298	NM_001241	Hs.37054	cyclin T2	4	40	4	1.2
	119307	BE048061	Hs.250895	ephrin-A3	3.3	571	171	2
	119367	T78324	Hs.53565	ribosomal protein L34	3.4	34	3	2.4
	119427	AW474547	Hs.92260	Homo sapiens PIG-M mRNA for mannosyltran	4.6	60	13	4.8
55	119580	AL079310	Hs.159225	high-mobility group protein 2-like 1	8.1	94	12	6.5
	119586	AF088033	Hs.56148	ESTs	3.3	33	8	0.9
	119638	NM_016122	Hs.57787	NY-REN-58 antigen	3.3	33	10	0.5
	119676	AA243837	Hs.57987	ESTs	5.4	54	1	4.1
	119717	AA918317	Hs.2533	B-cell CLL/lymphoma 11B (zinc finger pro	4.6	46	7	0.8
60	119771	AI905687	Hs.121281	EST	3.5	2073	595	2.1
	119780	NM_016625	Hs.43213	hypothetical protein	4.4	44	1	3.1
	119786	AL133396	Hs.58461	prion protein 2 (duplet)	3.4	34	1	2.5
	119805	AJ223810	Hs.58698	ESTs, Weakly similar to IEFS_HUMAN TRANS	3.6	36	1	2.9
	119859	AW245741	Hs.272531	ESTs, Weakly similar to A35659 knueppel-	5.2	52	6	1.8
65	119889	AI057404	Hs.14158	ESTs	3.7	37	4	1.9
	119940	AL050097	Hs.125019	DKFZP586B0319 protein	6.9	162	24	2.6
	119943	BE565849	Hs.153746	copine III	3.7	590	159	3.8
	120132	W57554	Hs.108787	lymphoid nuclear protein (LAF-4) mRNA	6.9	319	47	2.1
	120150	BE005771	Hs.101590	hypothetical protein FLJ22490	5.3	53	5	0.9
	120215	AF109219		phosphatidylinositol glycan, class N	3.2	106	34	3.3
	120260	AK000061		hypothetical protein	3.4	34	1	1.7

	120296	AW995911	Hs.299883	hypothetical protein FLJ23399	4.2	124	30	1.8
	120352	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypotheti	7.5	112	15	2.5
	120378	AA223249	Hs.285728	abl-interactor 12 (SH3-containing protel	3.3	33	10	2.8
	120418	AW986893	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (fr	4.8	48	1	0.5
5	120473	AA251973	Hs.269988	ESTs	3.4	34	4	0.1
	120493	AW968080	Hs.152939	Homo sapiens clone 24630 mRNA sequence	3.9	161	42	2
	120524	AA261852	Hs.192905	ESTs	6.8	68	1	0.2
	120554	AA284447	Hs.271887	ESTs	3.2	32	5	0.6
10	120562	BE244580	Hs.302267	hypothetical protein FLJ10330	8.5	127	15	1.6
	120571	AB037744	Hs.34892	KIAA1323 protein	3.7	37	1	0.5
	120572	H39599	Hs.294008	ESTs	3.6	36	8	0.2
	120588	AA703226	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586S211 (fr	5.6	101	18	1.6
	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	5.4	54	10	2.5
	120658	AI952639	Hs.98267	ESTs	3.2	32	8	3
15	120713	AW449855	Hs.96557	Homo sapiens cDNA FLJ12727 fis, clone NT	5.3	58	11	3.3
	120821	Y19062	Hs.96870	staufer (Drosophila, RNA-binding protein	3.3	33	3	0.2
	120822	AA347422	Hs.238040	EST, Weakly similar to B34087 hypothetic	3.8	38	7	0.2
	120915	AL135556	Hs.97104	ESTs	3.5	37	11	0.1
	120922	AA481003	Hs.97128	ESTs	3.1	31	1	0.4
20	120977	AA398155	Hs.97600	ESTs	7.9	79	1	2.7
	120999	AI972375	Hs.29626	hypothetical brain protein my038	5.1	51	1	2.4
	121125	AL042961	Hs.251278	KIAA1201 protein	3.7	37	10	1
	121176	AL121523	Hs.97774	ESTs	7	70	1	0.9
	121202	AA970946	Hs.97794	ESTs	3.9	39	1	0.2
25	121429	AA406293	Hs.41167	ESTs	3.4	34	1	0.8
	121448	AF044197	Hs.100431	B-cell attracting chemokine 1 (CXCL13;	3.5	35	1	2.6
	121463	AK000282	Hs.239681	hypothetical protein FLJ20275	10.3	103	1	9.3
	121517	AI002968	Hs.235402	ESTs, Weakly similar to T26525 hypotheti	3.5	143	41	2.6
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	4.6	46	3	0.8
30	121556	AA412494	Hs.98152	EST	4.2	77	19	1.4
	121581	AA416568		gb:zu05c10.s1 Soares_testis_NHT Homo sap	3.2	32	1	0.8
	121709	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	3.4	34	10	0.7
	121723	AA243499	Hs.104800	hypothetical protein FLJ10134	2.9	214	74	3.7
35	121831	AA449844	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	3.9	39	1	0.2
	121853	AA425887	Hs.98502	hypothetical protein FLJ14303	4.4	48	11	0.9
	121873	AV650929	Hs.145696	splicing factor (CC1.3)	3.6	150	42	3.2
	121913	AI249368	Hs.98558	ESTs; protease inhibitor 15 (PI15)	2.7	864	321	0.6
	121916	AW117207	Hs.98523	ESTs	3.5	35	3	2.3
	122004	AI810721	Hs.95424	ESTs	4.9	49	7	3.7
40	122063	AW794215	Hs.301226	KIAA1085 protein	3.2	88	28	1.2
	122223	AF169797	Hs.27413	adaptor protein containing pH domain, PT	12.6	126	7	7.5
	122235	AA436475	Hs.112227	membrane-associated nucleic acid binding	4.1	43	11	1.6
	122273	AI298368	Hs.150926	fucose-1-phosphate guanylyltransferase	3.1	31	1	1
	122383	AA446189	Hs.99051	ESTs	3.3	53	16	4
45	122507	BE567620	Hs.99210	ESTs	3.2	291	91	4
	122524	AA449453	Hs.192915	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1	31	6	0.8
	122636	AW651706	Hs.99519	hypothetical protein FLJ14007	3.5	35	1	3
	122637	AA454149	Hs.99357	EST	3.2	32	10	3.1
	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.2	36	11	2.5
50	122861	AA335721	Hs.119394	ESTs	5.6	108	20	1.8
	122873	AA749382	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	3.6	36	1	3.4
	122946	AI718702	Hs.308026	major histocompatibility complex, class	3.7	162	44	12.4
	122963	AA478446	Hs.69559	KIAA1096 protein	7.2	72	1	5.7
	122974	AA447871	Hs.194215	ESTs, Weakly similar to I38022 hypotheti	4.7	59	13	4.7
55	123016	AW338057	Hs.323231	Homo sapiens cDNA FLJ11946 fis, clone HE	3.3	207	63	3.5
	123090	AL135185	Hs.48778	riban protein	3.8	207	55	5.5
	123137	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	9.9	351	36	13.9
	123255	AA830335	Hs.105273	ESTs	4.1	72	18	1.5
	123284	AA488988	Hs.293796	ESTs	3.7	41	11	1.6
60	123442	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	6.7	67	2	2.1
	123449	AL049325	Hs.112493	Homo sapiens mRNA; cDNA DKFZp564D036 (fr	3.4	34	1	2.6
	123475	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098594, mRNA,	9.7	102	11	6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	4.2	42	7	2.9
	123503	AW975051	Hs.293166	ESTs, Weakly similar to I78885 serine/th	3.9	39	1	3.2
65	123516	AB037860	Hs.173933	nuclear factor I/A	4.3	43	1	3.5
	123518	AL035414	Hs.21068	hypothetical protein	5.8	58	1	4.9
	123523	AA608588		gb:ae54e06.s1 Stratagene lung carcinoma	3.1	927	295	2.1

	123527	AF150208	Hs.108327	damage-specific DNA binding protein 1 (1	5	121	25	5.9
	123570	AA608955	Hs.109653	ESTs	6.8	68	10	6.1
	123619	AA602964		gb:nc97c02.s1 NCL_CGAP_Pr2 Homo sapiens	8.5	85	1	4.3
5	123673	BE550112	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	3.9	39	5	3.7
	123709	AA706910	Hs.112742	ESTs	3.9	60	16	4.8
	123926	AA425769	Hs.227933	Alg5, S. cerevisiae, homolog of	3.4	80	24	3.8
	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	4.5	45	2	3.6
	124006	AI147155	Hs.270016	ESTs	5.8	321	55	17
10	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.4	880	85	5.3
	124287	H88296	Hs.5123	inorganic pyrophosphatase	3.1	41	14	2.7
	124292	H11341	Hs.13366	Homo sapiens cDNA: FLJ23567 fis, clone L	3.2	32	1	1.5
	124308	AA249027	Hs.241507	ribosomal protein S6	10.5	105	1	9.9
	124315	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom	12.8	141	11	12.2
15	124461	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	13.1	31	1	1.8
	124463	AI821780	Hs.179864	ESTs	3.3	33	1	1.7
	124677	R01073		gb:ye84c03.s1 Soares fetal liver spleen	4.2	42	7	3
	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.4	210	63	3.3
	124940	AF068846	Hs.103804	heterogeneous nuclear ribonucleoprotein	5.5	162	25	14.7
	125079	T90298	Hs.271396	ESTs	3.1	31	6	2.4
20	125091	T91518		gb:ye20f05.s1 Stratagene lung (937210) H	3.4	985	286	2.8
	125103	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro	3.6	224	63	4
	125144	A9037742	Hs.24336	KIAA1321 protein	6.3	63	6	5
	125150	W38240		Empirically selected from AFFX single pr	3.8	38	11	2.6
25	125156	W93048	Hs.250723	hypothetical protein MGC2747	3.1	31	1	2.8
	125226	AA782536	Hs.122647	N-myristoyltransferase 2	3.2	37	12	3.6
	125279	AW401809	Hs.4779	KIAA1150 protein	13.1	131	1	5.1
	125299	T32982	Hs.102720	ESTs	7.7	81	11	7.6
	125303	AA173319	Hs.288193	hypothetical protein MGC12217	14.3	143	9	13.1
	125377	W72949	Hs.77495	UBX domain-containing 1	3.3	34	11	3.2
30	125390	AL038165	Hs.75187	translocase of outer mitochondrial membr	8.2	124	15	11.5
	125471	AA421691	Hs.152601	UDP-glucose ceramide glucosyltransferase	3.7	224	61	21
	125617	AA287921	Hs.164950	ESTs	6.7	67	1	6
	125621	T62641	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	5.5	55	10	4.2
35	125628	AA418069	Hs.241493	natural killer-tumor recognition sequenc	5.5	63	12	1
	125660	AW292171	Hs.23978	scaffold attachment factor B	4.3	68	16	2.8
	125698	AF078847	Hs.191356	general transcription factor IIH, polype	4.8	48	5	4.1
	125745	AI858032	Hs.75722	ribophorin II	6.8	223	33	2.8
	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	8.3	87	11	0.4
40	125827	NM_003403	Hs.97496	YY1 transcription factor	11.3	124	11	9.7
	125852	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	10.6	306	4	26.5
	126349	T30968	Hs.13531	hypothetical protein FLJ10971	4.9	68	14	1.4
	126384	AW090198	Hs.4779	KIAA1150 protein	6.4	74	12	6.6
	126590	W78968	Hs.181307	H3 histone, family 3A	5	264	53	3.4
45	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.8	38	1	2.7
	126663	AW518478	Hs.181297	ESTs	3.6	36	6	2.9
	126695	AA643322	Hs.172028	a disintegrin and metalloproteinase doma	3.1	31	1	2.5
	126764	AA036755	Hs.102178	syntaxin 16	4.4	76	18	1
	126801	AW663887	Hs.7337	hypothetical protein FLJ10936	3.8	38	1	3
50	126813	AW163483	Hs.48320	double ring-finger protein, Dorrin	6.7	155	23	1.4
	126838	AL043489	Hs.279609	mitochondrial carrier homolog 2	8.8	110	13	10.5
	126855	AA129840	Hs.128065	ESTs	3.6	36	10	1.9
	126971	T26969	Hs.283664	aspartate beta-hydroxylase	5.5	79	15	4.4
	127167	AA625690	Hs.190272	ESTs	3.1	33	11	2.3
55	127251	AA936428	Hs.128638	ESTs	3.5	35	1	3.1
	127349	AA412108	Hs.269350	ESTs	4.8	108	22	1
	127439	D60237	Hs.14368	SH3 domain binding glutamic acid-rich pr	7.5	75	1	6.5
	127537	AI926047	Hs.162859	ESTs	3.8	38	7	3.4
	127542	AA703684	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN A	3.3	33	9	0.9
60	127677	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	4.3	152	35	12.5
	127774	AA313639	Hs.119488	cystein-rich hydrophobic domain 2	5.4	73	14	6.8
	127999	AW978827	Hs.69851	nucleolar protein family A, member 1 (H/	5.2	81	16	1.1
	128218	AA185733	Hs.292154	stromal cell protein	3.9	220	57	2.5
	128305	AI954968	Hs.279009	matrix Gla protein	9.4	94	3	5.3
65	128470	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	4.6	46	8	3.9
	128482	AI694143	Hs.296251	programmed cell death 4	7.2	72	1	5.8
	128501	AL133572	Hs.199009	protein containing CXXC domain 2	3.8	38	1	0.9
	128517	AW994403	Hs.100861	hypothetical protein FLJ14600	5.6	73	13	6.1

5	128530	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	4.2	104	25	7.8
	128579	N25956	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	3.1	172	55	3.1
	128595	U31875	Hs.272499	short-chain alcohol dehydrogenase family	3.3	105	32	3
	128610	N48373	Hs.10247	activated leucocyte cell adhesion molecu	7.3	106	15	5
	128653	D87432	Hs.10315	solute carrier family 7 (cationic amino	3.1	31	1	2.2
	128742	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	3.6	130	36	3.5
	128773	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.9	43	11	1.8
	128790	AF026692	Hs.105700	secreted frizzled-related protein 4	17.4	409	24	7.8
10	128793	AB011125	Hs.105749	KIAA0553 protein	3.1	34	11	2.7
	128794	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	3.6	36	5	1.5
	128835	AK001731	Hs.106390	Homo sapiens mRNA; cDNA DKFZp586f10924 (f	13.3	288	87	7.9
	128906	R57988	Hs.10706	epithelial protein lost in neoplasm beta	11.3	113	8	2.5
	128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	7.1	392	56	3.6
	128949	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	4.6	132	29	9.7
15	129017	AA115333	Hs.107968	ESTs	8.2	82	1	7.4
	129075	BE250162	Hs.83765	dihydrofolate reductase	5	50	1	3.3
	129095	L12350	Hs.108623	thrombospondin 2	3.2	814	257	2.4
	129151	N23018	Hs.171391	C-terminal binding protein 2	4.4	44	1	3.8
20	129168	AI132988	Hs.109052	chromosome 14 open reading frame 2	14.2	142	6	9.4
	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	7.1	71	1	6.2
	129243	BE169531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	5	64	13	6.3
	129259	AF220050	Hs.181385	uncharacterized hematopoietic stem/proge	5.2	75	15	6.4
	129278	NM_015344	Hs.11000	leptin receptor overlapping transcript-I	3.7	39	11	3.2
25	129337	NM_014918	Hs.110488	KIAA0990 protein	9.5	95	1	8.5
	129351	AL049538	Hs.62349	ras association (RalGDS/AF-6) domain con	7.6	92	12	1.4
	129366	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	7.1	150	21	14.5
	129393	BE219987	Hs.166982	phosphatidylinositol glycan, class F	3.9	54	14	5.1
	129457	X61959	Hs.207776	aspartylglucosaminidase	3.6	36	1	2.7
30	129496	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4	40	4	3.2
	129586	AW964541	Hs.11500	hypothetical protein FLJ21127	4.6	199	44	2.3
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.2	42	1	3.8
	129691	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.4	1111	175	5
	129698	BE242144	Hs.12013	ATP-binding cassette, sub-family E (OABP	4.8	48	8	3.8
35	129721	NM_001415	Hs.211539	eukaryotic translation initiation factor	5.8	171	30	2.9
	129740	BE165866	Hs.83623	nuclear receptor subfamily 1, group 1, m	4.5	45	1	2.4
	129755	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.3	53	9	3.6
	129801	R39246	Hs.239666	Homo sapiens cDNA FLJ13495 fis, clone PL	3.1	31	2	2.5
	129821	AB028945	Hs.12696	cortactin SH3 domain-binding protein	11.4	114	1	10
40	129869	AI222069	Hs.13015	hypothetical protein similar to mouse Dn	4.7	556	119	4.5
	129965	T71333	Hs.13854	ESTs	3.1	31	3	3
	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	3.2	32	1	0.2
	130036	BE061916	Hs.125849	chromosome 8 open reading frame 2	6.7	67	1	5.7
	130057	AF027153	Hs.324787	solute carrier family 5 (inositol transp	1	1	1	1
45	130095	AK001635	Hs.14838	hypothetical protein FLJ10773	14.6	219	15	7.6
	130115	T47294	Hs.149923	X-box binding protein 1	3.1	1336	434	1.4
	130170	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	5.3	53	9	3.2
	130173	U38847	Hs.151518	TAR (HIV) RNA-binding protein 1	4.2	46	11	1.1
	130343	AB040914	Hs.278628	KIAA1481 protein	13.2	331	25	12.4
50	130356	AF127577	Hs.155017	nuclear receptor interacting protein 1	3.3	354	108	4
	130367	AL135301	Hs.8768	hypothetical protein FLJ10849	8.1	81	9	5.5
	130385	AW067800	Hs.155223	stanniocalcin 2	72.2	722	1	1.9
	130407	BE385099	Hs.334727	hypothetical protein MGC3017	6.5	65	4	5.3
	130417	AW163518	Hs.155485	huntingtin interacting protein 2	3.5	79	23	2.5
55	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	6.1	61	1	5.7
	130455	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	10.8	706	66	9.2
	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	3.9	39	1	1.9
	130526	AW876523	Hs.15929	hypothetical protein FLJ12910	3.9	39	1	2.6
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	4.4	44	1	4.1
60	130604	AA383256	Hs.1657	estrogen receptor 1	32.2	322	1	4.7
	130614	AI354355	Hs.16697	down-regulator of transcription 1, TBP-b	5.2	251	48	21
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	10	100	1	7.6
	130619	AI963376	Hs.12532	chromosome 1 open reading frame 21	3.9	39	1	3.4
	130625	AF176012	Hs.260720	J domain containing protein 1	10.5	105	1	9
65	130677	AL161961	Hs.17767	KIAA1554 protein	6.8	129	19	12.1
	130681	R62676	Hs.17820	Rho-associated, coiled-coil containing p	4.1	41	1	3.6
	130693	R68537	Hs.17962	ESTs	9.2	234	26	16.8
	130712	AJ271881	Hs.279762	bromodomain-containing 7	17.5	175	2	12.8

	130723	BE247676	Hs.18442	E-1 enzyme	8.1	81	3	2.8
	130751	AF052105	Hs.18879	chromosome 12 open reading frame	4.9	49	1	4.3
	130780	AA197226	Hs.19347	hypothetical protein MGC11321	3.6	100	28	6.6
5	130863	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	3.4	525	154	5.3
	130871	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	10.5	121	12	1.6
	130888	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	6	202	34	3.7
	130974	NM_003528	Hs.2178	H2B histone family, member Q	7.1	100	14	7.5
	130979	NM_012446	Hs.169833	single-stranded-DNA-binding protein	3.2	87	27	1.7
10	130987	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	3.5	124	35	5.5
	130993	T97401	Hs.21929	ESTs	4.5	45	1	2.5
	131076	AA749230	Hs.26433	dolichyl-phosphate (UDP-N-acetylglucosam	3.2	210	66	3.8
	131085	BE207357	Hs.3454	KIAA1821 protein	3.8	42	11	0.6
	131126	NM_016156	Hs.181326	KIAA1073 protein	6.7	67	6	1.9
15	131129	BE541042	Hs.23240	Homo sapiens cDNA: FLJ21848 fis, clone H	5.8	115	20	2.5
	131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.8	585	153	3.7
	131164	AW013807	Hs.182265	keratin 19	5.2	1320	256	3.2
	131176	AA465113	Hs.23853	ESTs, Weakly similar to A34615 profilagg	3.8	38	1	3.3
	131200	BE540516	Hs.293732	hypothetical protein MGC3195	4.8	48	1	4.1
20	131216	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	6.1	343	56	16.4
	131245	AL080080	Hs.24766	thioredoxin domain-containing	8	100	13	2.9
	131248	AI038989	Hs.332633	Bardet-Biedl syndrome 2	4	95	24	1.1
	131273	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	4.6	239	53	3.5
	131319	NM_003155	Hs.25590	stannocalcin 1	3.5	402	114	2.1
25	131357	AI750575	Hs.173933	nuclear factor IIA	3.3	775	233	2.4
	131375	AW293165	Hs.143134	ESTs	3.8	38	1	3
	131379	AK001123	Hs.26176	hypothetical protein FLJ10261	3.9	116	30	0.5
	131388	NM_014810	Hs.92200	KIAA0480 gene product	7.6	76	1	5
	131475	AA992841	Hs.27263	KIAA1458 protein	5.1	113	22	6.1
30	131492	AI452601	Hs.288869	nuclear receptor subfamily 2, group F, m	8.4	169	20	4.6
	131501	AV661958	Hs.8207	GK001 protein	3.1	197	63	18.7
	131535	N22120	Hs.75277	hypothetical protein FLJ13910	5.9	59	1	4.4
	131544	AL355715	Hs.28555	programmed cell death 9 (PDCD9)	5.1	51	1	3.9
	131546	AA093688	Hs.28578	muscleblind (Drosophila)-like	3.8	79	21	6.9
35	131562	NM_003512	Hs.28777	H2A histone family, member L	4	350	88	3
	131564	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	4.7	381	81	6.4
	131604	AA306477	Hs.29379	hypothetical protein FLJ10687	4.6	46	7	3.6
	131684	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.2	82	26	6.6
	131687	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	6.7	93	14	8.4
	131689	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.8	51	14	1.7
40	131693	AW963776	Hs.110766	SAR1 protein	7.2	72	4	5.7
	131739	AF017986	Hs.31386	secreted frizzled-related protein 2	2.1	1561	757	1.7
	131742	AA961420	Hs.31433	ESTs	11.7	117	1	10.1
	131775	AB014548	Hs.31921	KIAA0648 protein	4.8	48	1	4.6
45	131787	D87077	Hs.195275	KIAA0240 protein	3.2	207	64	5.5
	131798	X86098	Hs.301449	adenovirus 5 E1A binding protein	3.4	115	34	9.1
	131835	W00712	Hs.32990	DKFZP566F084 protein	5.8	91	16	1.4
	131853	AI681917	Hs.3321	ESTs, Highly similar to IXX1_HUMAN IROQU	4.9	632	129	1.7
	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	6.8	68	1	5.6
	131881	AW361018	Hs.3383	upstream regulatory element binding prot	4	140	35	1.8
50	131885	BE502341	Hs.3402	ESTs	5.7	57	1	4.5
	131904	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	5.5	90	17	2.9
	131919	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	5.6	95	17	9.1
	131941	BE252983	Hs.35086	ubiquitin specific protease 1	7.4	103	14	6.5
55	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.7	37	1	3.4
	131949	AK000010	Hs.258798	hypothetical protein FLJ20003	3.5	35	1	2.5
	131965	W79283	Hs.35962	ESTs	5.5	168	31	4.4
	131977	U90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-di	3.7	37	9	2.8
	131985	AA503020	Hs.36563	hypothetical protein FLJ22418	40.2	402	1	4
60	131993	AI678910	Hs.3688	cisplatin resistance-associated overexpr	7.3	73	1	1.2
	132064	AA121098	Hs.3838	serum-inducible kinase	22.6	226	10	0.9
	132094	NM_018045	Hs.3945	CGI-107 protein	3.1	227	73	16.8
	132109	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	3.5	73	21	6.3
	132116	AW960474	Hs.40289	ESTs	3.6	141	39	12.6
65	132143	D52059	Hs.7972	KIAA0871 protein	4.9	49	1	4.1
	132160	W26406	Hs.295923	seven in absentia (Drosophila) homolog 1	4.4	53	12	2.1
	132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	5	225	45	9.1
	132180	NM_004480	Hs.418	fibroblast activation protein, alpha	10.7	433	41	7.2

	132197	AI699482	Hs.42151	ESTs	3.4	58	17	4
	132256	AI078345	Hs.431	murine leukemia viral (bmi-1) oncogene h	4.2	42	1	2.2
	132298	NM_015986	Hs.7120	cytokine receptor-like molecule 9	3.4	34	2	3
5	132316	U28831	Hs.44566	KIAA1641 protein	18.6	186	10	1.5
	132325	N37065	Hs.44856	hypothetical protein FLJ12116	5.5	323	59	10.5
	132358	NM_003542	Hs.46423	H4 histone family, member G	3.3	979	298	2.2
	132384	AA312135	Hs.46967	HSPCO34 protein	3.6	36	1	3.1
	132388	W32624	Hs.278626	Arg/Abi-Interacting protein ArgBP2	5.9	186	32	3.7
10	132393	AL136094	Hs.47334	hypothetical protein FLJ14495	4.2	159	38	7.1
	132407	BE613126	Hs.47783	B aggressive lymphoma gene	4.6	46	1	4.3
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.6	146	41	1.1
	132440	AB020699	Hs.112751	KIAA0892 protein	3.3	33	4	2.9
	132465	AW169847	Hs.49169	KIAA1634 protein	8.3	145	18	3.7
15	132522	AB023164	Hs.5070	KIAA0947 protein	4.6	46	1	4.4
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso	9.3	93	1	8.4
	132530	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S, c	4.9	49	1	4.4
	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	11.8	201	17	19.1
	132572	AI929659	Hs.237825	signal recognition particle 72kD	3.8	38	1	3
20	132592	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.8	93	20	3.1
	132602	AW606927	Hs.5306	hypothetical protein DKFZp586F1122 simil	6.1	61	2	5.9
	132616	BE262677	Hs.283558	hypothetical protein PRO1855	3.4	193	58	12.3
	132617	AF037335	Hs.5338	carbonic anhydrase XII	14.2	390	28	22.5
	132618	AL050025	Hs.279916	hypothetical protein FLJ20151	3.3	909	274	3.2
	132632	AU076916	Hs.5398	guanine monophosphate synthetase	5	50	1	4.1
25	132668	AB018319	Hs.5460	KIAA0776 protein	4.2	171	41	12.6
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	6.5	65	1	5.6
	132790	AW242243	Hs.168870	peroxisomal farnesylated protein	3.7	37	1	2.2
	132811	U25435	Hs.57419	CCCTC-binding factor (zinc finger protel	7	115	17	5.4
30	132852	AL120050	Hs.58220	Homo sapiens cDNA: FLJ23005 fis, clone L	3.3	61	19	5.1
	132856	NM_001448	Hs.58367	glypican 4	4.8	48	1	3.6
	132880	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	12.6	126	8	9.9
	132902	AI936442	Hs.59838	hypothetical protein FLJ10808	11	187	17	10.4
	132906	BE613337	Hs.234896	geminin	3.3	106	33	2.6
35	132914	AL047045	Hs.60293	Homo sapiens clone 122482 unknown mRNA	3.5	110	32	2.1
	132968	AF234532	Hs.61838	myosin X	4.1	62	15	4.9
	132977	AA093322	Hs.301404	RNA binding motif protein 3	22.1	221	9	17.8
	132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	12.7	311	25	2.4
	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3	380	127	5.5
40	133011	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	7.3	271	37	2.3
	133015	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.6	427	93	10.4
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.6	36	1	3.1
	133091	AK001628	Hs.64691	KIAA0483 protein	5.2	117	23	5
	133192	AA218564	Hs.67052	vacuolar protein sorting 26 (yeast homol	3.1	359	118	2.5
45	133197	AI275243	Hs.180201	hypothetical protein FLJ20671	5.1	58	12	5.7
	133199	AF231981	Hs.250175	homolog of yeast long chain polyunsatura	3	816	275	3.9
	133221	W32474	Hs.301746	RAP2A, member of RAS oncogene family	3.1	234	76	8.6
	133240	AK001489	Hs.242894	ADP-ribosylation factor-like 1	8.1	81	1	4.6
	133271	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	12.4	124	6	10.8
50	133291	BE297855	Hs.69855	NRAS-related gene	3.3	33	1	2.9
	133294	AJ001388	Hs.69997	zinc finger protein 238	7.9	234	30	18.9
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	4.6	46	5	3.5
	133362	AK001519	Hs.7194	CGI-74 protein	5	110	22	9.7
	133370	AF245505	Hs.72157	DKFZP564I1922 protein	3.2	725	227	3.2
55	133407	AF017987	Hs.7306	secreted frizzled-related protein 1	4.1	374	91	1.1
	133422	AB033061	Hs.73287	KIAA1235 protein	4.3	43	1	3.9
	133435	AI929357	Hs.323966	Homo sapiens clone H63 unknown mRNA	5.5	166	34	16.5
	133479	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.5	35	7	2.1
	133493	AW998046	Hs.194369	arginine-glutamic acid dipeptide (RE) re	3.6	39	11	0.4
60	133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	4.1	640	158	3
	133517	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	3.2	351	111	5.2
	133536	W25797	Hs.177486	amyloid beta (A4) precursor protein (pro	3.2	226	71	2.8
	133578	AU077050	Hs.75066	translin	3.4	178	53	8.8
	133633	D21262	Hs.75337	nucleolar and coiled-body phosphoprotein	4.7	47	1	4
65	133640	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	8.5	85	1	7.2
	133669	NM_006925	Hs.168975	splicing factor, arginine/serine-rich 5	3.6	36	1	0.4
	133681	AI352558	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-mo	3.4	234	68	10.7
	133746	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	9.3	93	1	7.8

	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.2	560	174	2.6
	133780	AA557660	Hs.73152	decorin	5.4	144	27	13.3
	133784	BE622743	Hs.301064	arlaptin 1	4.7	47	1	4.1
5	133814	NM_002462	Hs.76391	myxovirus (Influenza) resistance 1, homo	3.3	380	114	4.9
	133829	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	6.7	304	46	7.8
	133845	AA147026	Hs.76704	ESTs	6.2	600	97	4.1
	133913	AU076964	Hs.7753	calumenin	3.3	889	267	5
	133968	AA355986	Hs.232068	transcription factor 8 (represses Interl	3.7	91	25	2.6
10	133990	R48316	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564C1216 (f	3.4	91	27	6.5
	133999	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.8	78	1	5.6
	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	5.9	59	1	3.3
	134064	AF091622	Hs.78893	KIAA0244 protein	5.8	58	1	4.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	6.4	100	16	4.4
	134089	R51273	Hs.79029	ESTs	5.1	51	9	3.8
15	134095	NM_004354	Hs.79069	cyclin G2	5	50	1	3.2
	134098	BE513171	Hs.79086	mitochondrial ribosomal protein L3	4.8	246	51	3.9
	134110	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.5	1472	330	2.1
	134125	NM_014781	Hs.50421	KIAA0203 gene product	4.6	69	15	5.8
20	134246	D28459	Hs.80512	ubiquitin-conjugating enzyme E2A (RAD6 h	7	97	14	7.5
	134257	C05768	Hs.8078	Homo sapiens clone FBD3 Cri-du-chat crit	3.4	34	5	2.6
	134272	X76040	Hs.278614	protease, serine, 15	3.6	36	1	2.8
	134282	R45621	Hs.81057	hypothetical protein MGC2718	6.7	67	9	5.7
	134288	AI022650	Hs.8117	erbB2-interacting protein ERBIN	4.5	137	31	12
25	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	5.2	52	1	4.9
	134326	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	6.6	568	66	22.4
	134328	AW959281	Hs.8184	ESTs	4.8	53	11	3.7
	134348	AW291946	Hs.82065	interleukin 6 signal transducer (gp130,	7.1	71	4	6.4
	134359	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	3	68	23	2.8
30	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.4	44	1	4.1
	134374	N22687	Hs.8236	ESTs	13.3	445	34	6
	134380	AU077143	Hs.179565	minichromosome maintenance deficient (S.	4.5	45	2	3.4
	134395	AA455539	Hs.8262	lysosomal	6	60	5	5.9
	134401	AI916662	Hs.211577	kinesin 1 (kinesin receptor)	4.1	301	73	6.1
35	134405	AW067903	Hs.82772	collagen, type XI, alpha 1	4.6	1216	267	4.4
	134415	AI750762	Hs.82911	protein tyrosine phosphatase type IVA, m	4.9	163	34	15.1
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	4.9	49	3	3.8
	134419	W95642	Hs.82961	trefoil factor 3 (intestinal)	3.2	1872	592	3.3
	134421	AU077195	Hs.82985	collagen, type V, alpha 2	6.3	1075	171	3.8
40	134436	U29344	Hs.83190	fatty acid synthase	3.3	710	217	2
	134485	X82153	Hs.83942	cathepsin K (pycnodysostosis)	34.3	411	12	5.1
	134487	AF061739	Hs.83954	protein associated with PRK1	4.8	153	32	4.3
	134495	D63477	Hs.84087	KIAA0143 protein	3.1	147	48	12.7
	134520	BE091005	Hs.74861	activated RNA polymerase II transcriptio	3.3	33	1	2
45	134542	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi	4.2	42	5	2.6
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	3.9	39	1	2.5
	134590	AW903849	Hs.173840	HUEL (C4orf1)-interacting protein	3.7	41	11	0.6
	134604	NM_002864	Hs.865	RAP1A, member of RAS oncogene family	5.2	52	1	3
	134612	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	4.9	49	1	3.7
50	134643	AW299723	Hs.87223	bone morphogenetic protein receptor, typ	5.2	52	5	3.5
	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.4	64	1	5.1
	134656	AI750878	Hs.87409	thrombospondin 1	12.6	126	1	10.8
	134672	AF271212	Hs.322901	disrupter of silencing 10	5.4	81	15	2.6
	134700	AK000606	Hs.8868	golgi SNAP receptor complex member 1	3.4	179	52	1.5
55	134711	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.2	143	45	13.9
	134722	AF129536	Hs.284226	F-box only protein 6	7	70	6	6
	134856	BE281128	Hs.9030	TONDU	3.1	31	1	2.3
	134880	AI879195	Hs.90606	15 kDa selenoprotein	5.7	57	1	5
	134917	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	3.2	153	48	4.7
60	134921	AL137491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp434P1530 (f	4	452	114	2
	134982	AK002085	Hs.92308	Homo sapiens cDNA FLJ11223 fis, clone PL	5.1	150	30	7.2
	134989	AW966058	Hs.92381	nudix (nucleoside diphosphate linked moi	8.2	114	14	9.9
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase 7	11.5	115	1	10
	135035	AL034344	Hs.284186	forkhead box C1	5.4	259	48	1.4
65	135051	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.3	1296	394	2.2
	135062	AK000967	Hs.93872	KIAA1682 protein	3.8	240	64	3.2
	135073	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	6.1	101	13	7.9
	135098	AW274526	Hs.277721	ovarian carcinoma antigen CA125	3.3	33	1	2.6

	135117	W52493	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	5.3	53	1	4.1
	135144	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	7.4	74	5	2.4
	135154	AK001835	Hs.267812	sorting nexin 4	6.6	69	11	6.3
5	135155	AJ207958	Hs.168556	Homo sapiens, Similar to TEA domain faml	6.1	61	1	5.1
	135172	AB028956	Hs.12144	KIAA1033 protein	3.4	88	26	1.4
	135242	AI583187	Hs.9700	cyclin E1	3.1	31	1	2.3
	135243	BE463721	Hs.97101	putative G protein-coupled receptor	3.4	169	50	9.1
	135269	NM_003403	Hs.97495	YY1 transcription factor	3.4	475	142	2.5
	135356	BE312948	Hs.18104	hypothetical protein FLJ11274	3.1	31	10	1.7
10	135357	AI585004	Hs.79572	cathepsin D (lysosomal aspartyl) protease	4.7	710	151	2.5
	135389	U05237	Hs.99872	fetal Alzheimer antigen	20.6	206	4	19.1
	135397	L14922	Hs.168563	replication factor C (activator 1) 1 (14	3.2	32	1	2.4
	135400	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	3.2	117	37	9.4
15		AI471525	Hs.247486	ESTs	3.8	58	16	5.5
		X70683	Hs.93668	ESTs	1.8	1047	596	1.6
		L14922	Hs.82128	5T4 oncofetal trophoblast glycoprotein	5	285	58	1.2
		M23263	Hs.904	amylase-1;6-glucosidase; 4-alpha-glucanotransferase	3.1	31	1	2.6
		AI267866	Hs.148027	polymerase (RNA) II (DNA directed) polypeptide B	7.8	137	18	11.9
20		AA044840	Hs.241676	stromal cell-derived factor 1	4.7	114	25	0.9
		N90960	Hs.227459	ESTs; Moderately similar to !III ALU SUBFAMILY	4.7	151	32	9.3
		AA873285	Hs.137947	ESTs	4.7	47	3	4.4
		T56679	Hs.865	RAP1A; member of RAS oncogene family	4	40	1	3.4
		AA305536		"EST176522 Colon carcinoma (Caco-2) cell line II	3.6	121	34	11.8
25		AI369384		arylsulfatase D	3.5	113	33	1.7
		AA219081	Hs.242396	ESTs; Moderately similar to !III ALU SUBFAMILY]	3.4	107	32	9.9

TABLE 10A

Table 10 A shows the accession numbers for those pkeys lacking unigeneID's for Table 10. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
123619	371681_1	AA602964 AA609200
104602	524482_2	H47610 R86920
121581	283769_1	AA416568 AA442889 AA417233 AA442223
123523	genbank_AA608588	AA608588
100821	tigr_HT4306	M26460 U09116
125091	genbank_T91518	T91518
125150	NOT_FOUND_entrez_W38240	W38240
118475	genbank_N66845	N66845
104787	genbank_AA027317	AA027317
106055	genbank_AA417034	AA417034
113702	genbank_T97307	T97307
101046	entrez_K01160	K01160
101447	entrez_M21305	M21305
101624	entrez_M55998	M55998
124677	genbank_R01073	R01073
110581	genbank_H61560	H61560
119023	genbank_N98488	N98488
110775	genbank_N22414	N22414
112092	genbank_R44538	R44538
112253	genbank_R51818	R51818
107014	genbank_AA598820	AA598820
114988	genbank_AA251089	AA251089

TABLE 11: Figure 11 from BRCA 001-3 PCT

5 Table 11 depicts a preferred group of genes upregulated in tumor tissue compared to normal breast tissue.

10 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue
 R2: Ratio of 90th percentile tumor to normal body
 15 R3: Ratio of 75th percentile normal body to tumor
 R4: Ratio of tumor to normal breast tissue

20	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	R3	R4
	100131	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	13.2	244	19	9.9
	100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	15.7	1030	66	5
	100522	X51501	Hs.99949	prolactin-induced protein	22.7	760	34	1.4
	100666	L05424	Hs.169610	CD44 antigen (homing function and Indian	8.5	85	1	3.2
25	101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	15.3	153	1	14.1
	101478	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	9.6	96	1	8.5
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	9.4	94	1	0.3
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	8.9	89	5	8
	101888	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.3	73	1	5.3
30	102165	BE313280	Hs.159627	death associated protein 3	9.3	93	5	8
	102304	AF015224	Hs.46452	mammaglobin 1	8.5	2058	243	1.4
	102348	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	6.4	428	67	2.3
	102457	NM_001394	Hs.2359	dual specificity phosphatase 4	20.2	202	5	1.3
	102567	U63830	Hs.146847	TRAF family member-associated NFKB activ	8.2	82	1	6.8
35	102823	D85390	Hs.5057	carboxypeptidase D	5.6	56	1	5.3
	103557	AL133415	Hs.297753	vimentin	7.5	136	18	3.4
	103613	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	7.3	73	1	5.2
	104115	AF183810	Hs.26102	opposite strand to trichorhinophalangeal	29	290	1	26.8
	104657	AI239923	Hs.30098	ESTs	14.9	149	1	6.4
40	104804	AI858702	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	7.7	77	1	5.1
	104807	AI139058	Hs.125790	leucine-rich repeat-containing 2	7	70	1	6.5
	104896	AW015318	Hs.23165	ESTs	7.4	74	1	6
	104943	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	16.2	162	1	4.2
	105038	AW503733	Hs.9414	KIAA1488 protein	5.5	55	1	5.2
45	105329	AA234561	Hs.22862	ESTs	2.8	131	47	3.9
	105500	AW602166	Hs.222399	CEGP1 protein	25.4	508	20	3
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	8.3	83	3	1.8
	105730	AW377314	Hs.5364	DKFZP564I052 protein	6.9	69	1	4.4
	106012	AI240665	Hs.8895	ESTs	21.2	212	6	17.4
50	106095	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	26.3	358	14	1
	106155	AA425414	Hs.33287	nuclear factor I/B	9.9	483	49	1.8
	107102	AB037765	Hs.30652	KIAA1344 protein	6.3	63	1	5.4
	107136	AV661858	Hs.8207	GK001 protein	2.5	392	155	4.3
	107151	AW378065	Hs.8687	ESTs	15.6	156	7	10.8
55	107922	BE153855	Hs.61460	Ig superfamily receptor LNIR	9	90	1	5.5
	108339	AW151340	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	18.7	187	1	17
	109112	AW419196	Hs.257924	hypothetical protein FLJ13782	4.1	334	82	3.4
	109292	AW975746	Hs.188662	KIAA1702 protein	7.1	71	1	6.5
	109415	U80736	Hs.110826	trinucleotide repeat containing 9	12.3	123	1	11.3
60	109912	AW390822	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	14.2	142	1	9.5
	110009	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	6.3	693	110	7.2
	110915	BE092285	Hs.29724	hypothetical protein FLJ13187	20.9	209	1	19.5
	111164	N46180	Hs.122489	Homo sapiens cDNA FLJ13289 fis, clone OV	7.7	77	1	5

	111179	AK000136	Hs.10760	asporin (LRR class 1)	25.1	288	12	6.7
	111190	AK002055	Hs.151046	hypothetical protein FLJ11193	6.3	63	1	5.8
	111223	AA852773	Hs.334838	KIAA1866 protein	3.6	402	112	4.9
	111357	BE314949	Hs.67128	hypothetical protein FLJ23309	3.8	425	111	4
5	112244	AB029000	Hs.70823	KIAA1077 protein	5.7	567	100	6.7
	113047	AI571940	Hs.7549	ESTs	9.6	124	13	9
	113702	T97307		gb:ye53h05.s1 Soares fetal liver spleen	12.3	129	11	11.7
	114124	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	24.2	242	10	5.6
	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	6.7	67	1	6.3
10	114768	AF212848	Hs.182339	ets homologous factor	13.7	137	1	8.9
	114860	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.1	91	1	7.6
	114965	AI733881	Hs.72472	BMP-R1B	35.9	359	10	29.7
	114988	AA251089		gb:zs04f05.s1 NCLCGAP_GCB1 Homo sapiens	11.5	115	1	6.9
	115206	AW183695	Hs.186572	ESTs	5.8	58	1	5
15	115719	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	7.6	144	19	13.9
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	6.2	62	1	5.4
	116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	1.8	1047	596	1.6
	116786	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	22.8	228	9	12.4
	117280	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C	3.9	322	83	4.4
20	117412	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	17.4	174	9	6.9
	118472	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	14.5	145	1	2.4
	119271	AI051118	Hs.65328	Fanconi anemia, complementation group F	8.2	82	1	6.4
	119771	AI905687	Hs.2533	EST	3.5	2073	595	2.1
	120562	BE244580	Hs.302267	hypothetical protein FLJ10330	8.5	127	15	1.6
25	121463	AK000282	Hs.239681	hypothetical protein FLJ20275	10.3	103	1	9.3
	121723	AA243499	Hs.104800	hypothetical protein FLJ10134	2.9	214	74	3.7
	122963	AA478446	Hs.69559	KIAA1096 protein	7.2	72	1	5.7
	123137	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	9.9	351	36	13.9
	123619	AA602964		gb:nc97c02.s1 NCLCGAP_Pr2 Homo sapiens	8.5	85	1	4.3
30	123709	AA706910	Hs.112742	ESTs	3.9	60	16	4.8
	124006	AI147155	Hs.270016	ESTs	5.8	321	55	17
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.4	880	85	5.3
	124308	AA249027	Hs.241507	ribosomal protein S6	10.5	105	1	9.9
	125279	AW401809	Hs.4779	KIAA1150 protein	13.1	131	1	5.1
35	125617	AA287921	Hs.164950	ESTs	6.7	67	1	6
	127439	D60237	Hs.14368	SH3 domain binding glutamic acid-rich pr	30.6	306	4	26.5
	128305	AI954968	Hs.279009	matrix Gla protein	7.5	75	1	6.5
	128482	AI694143	Hs.296251	programmed cell death 4	7.2	72	1	5.8
	128790	AF026692	Hs.105700	secreted frizzled-related protein 4	17.4	409	24	7.8
40	128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	7.1	392	56	3.6
	129017	AA115333	Hs.107968	ESTs	8.2	82	1	7.4
	129229	AF013758	Hs.109843	polyadenylate binding protein-interactin	7.1	71	1	6.2
	129337	NM_014918	Hs.110488	KIAA0990 protein	9.5	95	1	8.5
	129366	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	7.1	150	21	14.5
45	129821	AB028945	Hs.12696	cortactin SH3 domain-binding protein	11.4	114	1	10
	130036	BE061916	Hs.125849	chromosome 8 open reading frame 2	6.7	67	1	5.7
	130057	AF027153	Hs.324787	solute carrier family 5 (inositol transp	1	1	1	1
	130095	AK001635	Hs.14838	hypothetical protein FLJ10773	14.6	219	15	7.6
	130343	AB040914	Hs.278628	KIAA1481 protein	13.2	331	25	12.4
50	130385	AW067800	Hs.155223	stanniocalcin 2	72.2	722	1	1.9
	130407	BE385039	Hs.334727	hypothetical protein MGC3017	6.5	65	4	5.3
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	6.1	61	1	5.7
	130455	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	10.8	706	66	9.2
	130604	AA383256	Hs.1657	estrogen receptor 1	32.2	322	1	4.7
55	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	10	100	1	7.6
	130712	AJ271881	Hs.279762	bromodomain-containing 7	17.5	175	2	12.8
	131148	AW953575	Hs.303125	p53-induced protein PIGPC1	3.8	585	153	3.7
	131388	NM_014810	Hs.92200	KIAA0480 gene product	7.6	76	1	5
	131584	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	4.7	381	81	6.4
60	131742	AA961420	Hs.31433	ESTs	11.7	117	1	10.1
	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	6.8	68	1	5.6
	131985	AA503020	Hs.36563	hypothetical protein FLJ22418	40.2	402	1	4
	132316	U28831	Hs.44566	KIAA1641 protein	18.6	186	10	1.5
	132528	T78736	Hs.50758	SMC4 (structural maintenance of chromoso	9.3	93	1	8.4
65	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	6.5	65	1	5.6
	132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	12.7	311	25	2.4
	133015	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.6	427	93	10.4

5	133199	AF231981	Hs.250175	homolog of yeast long chain polyunsatura	3	816	275	3.9
	133240	AK001489	Hs.242894	ADP-ribosylation factor-like 1	8.1	81	1	4.8
	133271	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	12.4	124	6	10.8
	133640	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	8.5	85	1	7.2
	133746	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	9.3	93	1	7.8
10	133999	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.8	78	1	5.6
	134110	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.5	1472	330	2.1
	134485	X82153	Hs.83942	cathepsin K (pseudosostosis)	34.3	411	12	5.1
	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.4	64	1	5.1
	134880	AI879195	Hs.90606	15 kDa selenoprotein	5.7	57	1	5
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase 7	11.5	115	1	10
	135389	U05237	Hs.99872	fetal Alzheimer antigen	20.6	206	4	19.1
	128305	AI954968	Hs.279009	matrix Gla protein	9.4	94	3	5.3

TABLE 11A

Table 11A shows the accession numbers for those pkeys lacking unigeneID's for Table 11. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
123619	371681_1	AA602964 AA609200
113702	genbank_T97307	T97307
114968	genbank_AA251089	AA251089

TABLE 12: Figure 12 from BRCA 001-3 PCT

- 5 **Table 12 depicts a preferred group of genes upregulated in tumor tissue compared to normal breast tissue.**

10	Pkey:	Unique Eos probeset identifier number						
	ExAccn:	Exemplar Accession number, Genbank accession number						
	UnigenelD:	Unigene number						
	Unigene Title:	Unigene gene title						
15	R1:	Ratio of tumor to normal body tissue						
	R2:	Ratio of 90 th percentile tumor to body						
	R3:	Ratio of 75 th percentile body to tumor						
	R4:	Ratio of tumor to normal breast tissue						
<hr/>								
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3	R4
20	100131	D12485	Hs.11951	phosphodiesterase I (PC-1)	13.2	244	19	9.9
	105500	AW602166	Hs.222399	ESTs	25.4	508	20	3
	112244	AB029000	Hs.70823	KIAA1077 protein	5.7	567	100	6.7
	114124	W57554	Hs.125019	ESTs	24.2	242	10	5.6
25	119771	AI905687	Hs.2533	ESTs	3.5	2073	595	2.1
	121723	AA243499	Hs.104800	ESTs	2.9	214	74	3.7
	128790	AF026692	Hs.105700	secreted frizzled-related protein 4	17.4	409	24	7.8
	131148	AW953575	Hs.303125	ESTs	3.8	585	153	3.7
	131985	AA503020	Hs.36563	ESTs	40.2	402	1	4
	133199	AF231981	Hs.250175	Homo sapiens clone 23904 mRNA sequence	3	816	275	3.9

TABLE 13: Table 1 from BRCA 001-5 US

5 Table 13 depicts a preferred group of genes upregulated in breast cancer cells.

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal body tissue			
15					
20	Pkey	ExAccn	UniGene ID	Unigene Title	R1
	100038	M97935		control	16.7
	100039	M97935		control	6.3
	100040	M97935		control	8.3
	100041	M97935		control	14.8
25	100082	AB003103	Hs.4295	proteasome (prosome; macropain) 26S sub	7.5
	100091	AF000177	Hs.111783	Lsm1 protein	4.9
	100100	AF006084	Hs.11538	actin related protein 2/3 complex; subunit	4.7
	100103	AF007875	Hs.5085	dolichyl-phosphate mannosyltransferase p	13.4
	100114	D00596	Hs.82962	thymidylate synthetase	15.9
30	100121	D10495	Hs.155342	protein kinase C; delta	4.6
	100123	D10523	Hs.168669	oxoglutarate dehydrogenase (lipoamide)	7.5
	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S sub	4.4
	100131	D12485	Hs.11951	phosphodiesterase 1/nucleotide pyrophosp	8.7
	100137	D13627	Hs.15071	chaperonin containing TCP1; subunit 8 (t	9.5
35	100144	D13643	Hs.75616	Human mRNA for KIAA0018 gene; comp	6
	100147	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin I-like	8.5
	100154	D14657	Hs.81892	KIAA0101 gene product	10.5
	100164	D14812	Hs.173714	MORF-related gene X	4.6
	100169	D14878	Hs.82043	D123 gene product	7.9
40	100190	D21090	Hs.178658	RAD23 (S. cerevisiae) homolog B	5.6
	100203	D25538	Hs.172199	adenylate cyclase 7	9.9
	100209	D26308	Hs.76289	biliverdin reductase B (flavin reductase (N	4.9
	100215	D26598	Hs.82793	proteasome (prosome; macropain) subunit	14.2
	100216	D26599	Hs.1390	proteasome (prosome; macropain) subunit	11.3
45	100219	D28137	Hs.118110	bone marrow stromal cell antigen 2	5.7
	100227	D28915	Hs.82316	interferon-induced; hepatitis C-associated	5.7
	100248	D31888	Hs.78398	KIAA0071 protein	7.4
	100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	5.6
	100294	D49396	Hs.75454	antioxidant protein 1	12.9
50	100307	D50525	Hs.699	hypothetical protein	8.4
	100335	D63391	Hs.6793	platelet-activating factor acetylhydrolase;	6.8
	100340	D63487	Hs.82563	KIAA0153 protein	4.4
	100355	D78129	Hs.71465	Homo sapiens mRNA for squalene epoxid	12.6
	100363	D78514	Hs.78563	ubiquitin-conjugating enzyme E2G 1 (hom	4.6
55	100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homolo	6.5
	100372	D79987	Hs.184339	KIAA0175 gene product	8.4
	100375	D80004	Hs.75909	KIAA0182 protein	4.5
	100379	D82060	Hs.278721	Ke4 gene; mouse; human homolog of	8.1
	100387	D83777	Hs.75137	KIAA0193 gene product	10.7
60	100393	D84145	Hs.39913	novel RGD-containing protein	7.2
	100398	D84557	Hs.155462	minichromosome maintenance deficient (m	7.2
	100405	D86425	Hs.82733	nidogen 2	5.4
	100406	D86479	Hs.118397	AE-binding protein 1	4.3
	100409	D86957	Hs.80712	KIAA0202 protein	11.9
65	100421	D86985	Hs.79276	Human mRNA for KIAA0232 gene; comp	9.7
	100446	D87464	Hs.10037	KIAA0274 gene product	6.4
	100447	D87465	Hs.74583	KIAA0275 gene product	10
	100448	D87469	Hs.57652	EGF-like-domain; multiple 2	6.2

	100467	D89052	Hs.7476	ATPase; H ⁺ transporting; lysosomal (vacu	7.5
	100468	D89289	Hs.118722	fucosyltransferase 8 (alpha (1;6) fucosyltr	5
	100486	HT1112	Hs.10842	Ras-Like Protein Tc4	16.9
5	100497	HT1400	Hs.79137	Carboxyl Methyltransferase, Aspartate, A	5.6
	100618	HT2710	Hs.114599	Collagen, Type VII, Alpha 1	7.5
	100661	HT3018	Hs.132748	Ribosomal Protein L39 Homolog	4.4
	100667	HT3127	Hs.169610	Epican, Alt. Splice 11	4.6
	100668	HT3938	Hs.169610	Epican, Alt. Splice 12	4.4
	100676	HT3742	Hs.287820	Fibronectin, Alt. Splice 1	9
10	100775	HT26388	Hs.89603	Mucin 1, Epithelial, Alt. Splice 9	4.7
	100783	HT4018	Hs.191356	Basic Transcription Factor, 44 Kda Subun	13.7
	100829	HT4343	Hs.278544	Cytosolic Acetoacetyl-Coenzyme A Thio	10.6
	100830	HT4344	Hs.4756	Rad2	5.5
	100840	HT4392	Hs.183418	Protein Kinase Pilsre, Alpha, Alt. Splice	4.1
15	100850	HT417	Hs.297939	Cathepsin B	4
	100866	HT4582	Hs.75113	Transcription Factor Iiia	4.9
	100906	HT5158	Hs.5398	Guanosine 5'-Monophosphate Synthase	8.7
	100914	HT511	Hs.324178	Ras Inhibitor Inf	7.2
	100918	HT544	Hs.73946	Endothelial Cell Growth Factor 1	5.9
20	100945	HT884	Hs.180686	Oncogene E6-Ap, Papillomavirus	4.6
	100975	J02923	Hs.76506	lymphocyte cytosolic protein 1 (L-plastin	30.1
	100988	J03589	Hs.76480	ubiquitin-like 4	8.3
	100996	J03809	Hs.14623	Interferon; gamma-inducible protein 30	6.9
	100999	J03934	Hs.80706	diaphorase (NADH/NADPH) (cytochrom	4.3
25	101011	J04430	Hs.1211	acid phosphatase 5; tartrate resistant	5.9
	101017	J04599	Hs.821	biglycan	5.1
	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B;	37.2
	101038	J05249	Hs.79411	replication protein A2 (32kD)	6.1
	101054	K02405	Hs.73931	Human MHC class II HLA-DQ-beta mRNA	4.3
30	101061	K03515	Hs.180532	glucose phosphate isomerase	4.3
	101091	L06132	Hs.149155	voltage-dependent anion channel 1	7.4
	101097	L06797	Hs.89414	chemokine (C-X-C motif); receptor 4 (fus	4.6
	101104	L07615	Hs.169266	Human neuropeptide Y receptor Y1 (NPY	18.3
	101143	L12723	Hs.90093	heat shock 70kD protein 4	17.4
35	101152	L13800	Hs.9884	Homo sapiens liver expressed protein gen	7.6
	101183	L19779	Hs.795	H2A histone family; member O	10.9
	101216	L25876	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	7.4
	101233	L29008	Hs.878	sorbitol dehydrogenase	14.6
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	7.5
40	101282	L36810	Hs.79387	proteasome (prosome; macropain) 26S sub	4.4
	101326	L42572	Hs.78504	inner membrane protein; mitochondrial (m	5.8
	101332	L47276	Hs.156346	Homo sapiens (cell line HL-6) alpha topo	18.9
	101348	L77213	Hs.30954	phosphomevalonate kinase	7.5
	101352	L77701	Hs.16297	COX17 (yeast) homolog; cytochrome c ox	9.3
45	101378	M13755	Hs.833	interferon-stimulated protein; 15 kDa	18.1
	101395	M15796	Hs.78996	proliferating cell nuclear antigen	8.6
	101404	M16342	Hs.182447	heterogeneous nuclear ribonucleoprotein C	4.5
	101439	M20902	Hs.268571	apolipoprotein C-I	6.1
	101464	M22538	Hs.51299	NADH dehydrogenase (ubiquinone) flavo	8.7
50	101469	M22877	Hs.169248	Human somatic cytochrome c (HCS) gene	4.2
	101472	M22960	Hs.118126	protective protein for beta-galactosidase (6.5
	101478	M23379	Hs.758	RAS p21 protein activator (GTPase activa	14
	101484	M24594	Hs.20315	Interferon-induced protein 56	9.2
	101539	M30818	Hs.926	myxovirus (influenza) resistance 2; homoi	5.1
55	101540	M30938	Hs.84981	X-ray repair complementing defective rep	4.7
	101544	M31169		Human propionyl-CoA carboxylase beta-s	5.5
	101552	M31642	Hs.82314	hypoxanthine phosphoribosyltransferase 1	8.5
	101580	M34677	Hs.83363	DNA segment on chromosome X (unique)	4.5
	101600	M37583	Hs.119192	H2A histone family; member Z	5.7
60	101663	M60750	Hs.2178	H2B histone family; member A	5.8
	101684	M60752	Hs.121017	H2A histone family; member A	13.5
	101687	M60858	Hs.79110	nucleolin	4
	101684	M63256	Hs.75124	cerebellar degeneration-related protein (62	7.6
	101702	M64929	Hs.179574	protein phosphatase 2 (formerly 2A); regu	4.2
65	101754	M77142	Hs.239489	TIA1 cytotoxic granule-associated RNA-b	4.5
	101768	M77836	Hs.79217	pyrroline-5-carboxylate reductase 1	5.7
	101767	M81057	Hs.180884	carboxypeptidase B1 (tissue)	21.7

	101770	M81601	Hs.78869	transcription elongation factor A (SII); 1	4.6
	101791	M83822	Hs.62354	cell division cycle 4-like	9.7
	101803	M86546	Hs.155691	pre-B-cell leukemia transcription factor 1	5.5
5	101809	M86849	Hs.323733	Homo sapiens connexin 26 (GJB2) mRNA	22.5
	101839	M93036	Hs.692	membrane component; chromosomal 4; su	4
	101851	M94250	Hs.82045	midline (neurite growth-promoting factor	7.6
	101888	M99701	Hs.95243	transcription elongation factor A (SII)-like	11.4
	101973	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:po	4.6
	101991	U00938	Hs.166	Human SREBP-1 mRNA; complete cds	4.1
10	102009	U02680	Hs.82643	protein tyrosine kinase 9	4.4
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer; n	4
	102047	U07158	Hs.83734	syntaxin 4A (placental)	6.1
	102051	U07550	Hs.1197	heat shock 10kD protein 1 (chaperonin 10	4.4
	102083	U10323	Hs.75117	interleukin enhancer binding factor 2; 45k	10.4
15	102095	U11313	Hs.75760	sterol carrier protein 2	9.5
	102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	6.6
	102133	U15173	Hs.155596	BCL2/adenovirus E1B 19kD-interacting p	4.3
	102148	U16954	Hs.75823	ALL1-fused gene from chromosome 1q	6.9
	102179	U19713	Hs.76364	allograft inflammatory factor 1	4.8
20	102180	U19718	Hs.83551	microfibrillar-associated protein 2	7.2
	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin; b	7.2
	102198	U21090	Hs.74598	polymerase (DNA directed); delta 2; regu	4.3
	102202	U21931	Hs.574	fructose-bisphosphatase 1	4.5
25	102209	U22970	Hs.265827	interferon; alpha-inducible protein (cine	9.9
	102211	U23070	Hs.78776	putative transmembrane protein	4.9
	102220	U24389	Hs.65436	lysyl oxidase-like 1	8.5
	102224	U24704	Hs.148495	proteasome (prosome; macropain) 26S sub	5.4
	102234	U26312	Hs.278554	chromobox homolog 3 (Drosophila HP1 g	7.7
	102250	U26014	Hs.74122	caspase 4; apoptosis-related cysteine prot	5.4
30	102260	U28386	Hs.159557	karyopherin alpha 2 (RAG cohort 1; impo	6.3
	102261	U28488	Hs.155935	complement component 3a receptor 1	5.7
	102273	U30888	Hs.75981	ubiquitin specific protease 14 (trNA-guan	6.1
	102298	U32849	Hs.54483	N-myc (and STAT) interactor	4.1
	102302	U33052	Hs.69171	protein kinase C-like 2	4.3
35	102305	U33288	Hs.90073	chromosome segregation 1 (yeast homolog	5.4
	102320	U34683	Hs.82327	glutathione synthetase	4.1
	102330	U35451	Hs.77254	chromobox homolog 1 (Drosophila HP1 b	4
	102346	U37519	Hs.87539	aldehyde dehydrogenase 8	9.4
40	102361	U39400	Hs.75859	chromosome 11 open reading frame 4	5.2
	102362	U39412	Hs.75932	N-ethylmaleimide-sensitive factor attachm	9.3
	102369	U39840	Hs.299867	hepatocyte nuclear factor 3; alpha	7.7
	102395	U41767	Hs.92208	a disintegrin and metalloproteinase domai	10.4
	102409	U43286	Hs.118725	selenophosphate synthetase 2	6.2
45	102418	U43923	Hs.79058	suppressor of Ty (S.cerevisiae) 4 homolog	4.1
	102425	U44772	Hs.3873	palmitoyl-protein thioesterase (ceroid-lipo	4.8
	102457	U48807	Hs.2359	dual specificity phosphatase 4	6.3
	102465	U49352	Hs.81548	2;4-dienoyl CoA reductase 1; mitochondri	9.4
	102495	U51240	Hs.79356	Lysosomal-associated multispinning mem	6.5
50	102534	U56833	Hs.198307	von Hippel-Lindau binding protein 1	8.6
	102546	U57877	Hs.3577	succinate dehydrogenase complex; subuni	4.3
	102549	U58046	Hs.198899	eukaryotic translation initiation factor 3; s	6.3
	102557	U58766	Hs.264428	tissue specific transplantation antigen P35	5
	102562	U59309	Hs.75653	fumarate hydratase	6
	102568	U59877	Hs.223025	RAB31; member RAS oncogene family	9.1
55	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatid	7.9
	102581	U61145	Hs.77256	enhancer of zeste (Drosophila) homolog 2	7.6
	102590	U62136	Hs.79300	Homo sapiens enterocyte differentiation a	7
	102591	U62325	Hs.324125	amyloid beta (A4) precursor protein-blind	4
	102592	U62389	Hs.11223	Human putative cytosolic NADP-depende	5
60	102617	U65928	Hs.198767	Jun activation domain binding protein	6.1
	102618	U65932	Hs.81071	extracellular matrix protein 1	23.2
	102638	U67319	Hs.9216	caspase 7; apoptosis-related cysteine prot	8.9
	102663	U70322	Hs.168075	karyopherin (importin) beta 2	7.1
	102666	U70660	Hs.279910	ATX1 (antioxidant protein 1; yeast) homo	4.7
65	102679	U72681	Hs.11342	ninjurin 1; nerve injury-induced protein-1	4.7
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	7.7
	102704	U76638	Hs.54089	BRCA1 associated RING domain 1	5.6

	102705	U77180	Hs.50002	small inducible cytokine subfamily A (Cy	11.8
	102721	U79241	Hs.118666	Human clone 23759 mRNA; partial cds	15
	102729	U79254	Hs.181311	asparaginyl-tRNA synthetase	5
5	102739	U79282	Hs.155572	Human clone 23801 mRNA sequence	6
	102742	U79293	Hs.159264	Human clone 23948 mRNA sequence	13.1
	102761	U82130	Hs.118910	tumor susceptibility gene 101	7
	102788	U86602	Hs.74407	nucleolar protein p40	4.1
	102790	U87269	Hs.154196	E4F transcription factor 1	7.1
	102801	U89606	Hs.38041	pyridoxal (pyridoxine; vitamin B6) kinase	4.7
10	102808	U90426	Hs.179606	nuclear RNA helicase; DECD variant of D	7.5
	102817	U90904	Hs.83724	Human clone 23773 mRNA sequence	15.2
	102823	U90914	Hs.5057	carboxypeptidase D	6.6
	102827	U91327	Hs.6456	chaperonin containing TCP1; subunit 2 (b	6
	102838	U94592	Hs.80658	Human uncoupling protein homolog (UCP	6.1
15	102841	U95006	Hs.37616	Human D9 splice variant B mRNA; comp	4.2
	102844	U96113	Hs.324275	Homo sapiens Nedd-4-like ubiquitin-prot	6.8
	102868	X02419	Hs.77274	plasminogen activator; urokinase	4
	102907	X08985	Hs.202833	heme oxygenase (decycling) 1	22.7
	102919	X12447		aldolase A; fructose-bisphosphate	9.9
20	102929	X13238	Hs.74649	cytochrome c oxidase subunit VIc	5.4
	102973	X16663	Hs.14601	hematopoietic cell-specific Lyn substrate	4.8
	102983	X17620	Hs.118638	non-metastatic cells 1; protein (NM23A)	4.6
	102985	X17644	Hs.2707	G1 to S phase transition 1	20.6
	103003	X52003	Hs.1406	trefoil factor 1 (breast cancer; estrogen-ind	10.7
25	103018	X53296	Hs.81134	interleukin 1 receptor antagonist	5.8
	103023	X53793	Hs.117950	multifunctional polypeptide similar to SA	4
	103036	X54925	Hs.83169	matrix metalloproteinase 1 (interstitial col	7.3
	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	17.8
	103073	X59417	Hs.74077	proteasome (prosome; macropain) subunit	5.6
30	103075	X59543	Hs.2934	ribonucleotide reductase M1 polypeptide	4.2
	103080	X59798	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomat	6.7
	103094	X60787	Hs.296281	interleukin enhancer binding factor 1	5.7
	103105	X61970	Hs.76913	proteasome (prosome; macropain) subunit	5.8
	103121	X63679	Hs.4147	translocating chain-associating membrane	4.2
35	103149	X66363	Hs.171834	PCTAIRE protein kinase 1	12
	103180	X69433	Hs.5337	isocitrate dehydrogenase 2 (NADP+); mit	18.9
	103182	X69819	Hs.99995	intercellular adhesion molecule 3	10.7
	103188	X70040	Hs.2942	macrophage stimulating 1 receptor (c-met	4.1
	103191	X70218	Hs.2903	protein phosphatase 4 (formerly X); cataly	10.7
40	103193	X70476	Hs.75724	coatamer protein complex; subunit beta 2	8.2
	103194	X70649	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box pol	13.7
	103195	X70940	Hs.2842	eukaryotic translation elongation factor 1	13.4
	103206	X72755	Hs.77367	monokine induced by gamma interferon	15.1
	103207	X72790		Human endogenous retrovirus mRNA for	5.3
45	103208	X72841	Hs.31314	retinoblastoma-binding protein 7	12.3
	103216	X74262	Hs.16003	retinoblastoma-binding protein 4	4.1
	103226	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral onco	6.9
	103230	X75861	Hs.74637	testis enhanced gene transcript	7.9
	103282	X78565	Hs.269114	hexabrachion (tenascin C; cytactin)	5
50	103278	X79882	Hs.80680	lung resistance-related protein	5.7
	103297	X81788	Hs.9078	immature colon carcinoma transcript 1	4.6
	103302	X82103	Hs.3059	coatamer protein complex; subunit beta	4.5
	103316	X83301	Hs.324728	SMA5	7.1
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypepti	4
55	103349	X89059		serine/threonine kinase 9	4.7
	103352	X89398	Hs.78853	uracil-DNA glycosylase	5.3
	103364	X90872	Hs.279929	SULT1C sulfotransferase	4
	103374	X91788	Hs.84974	chloride channel; nucleotide-sensitive; 1A	4.2
	103380	X92396	Hs.24167	synaptobrevin-like 1	13.6
60	103395	X94754	Hs.279946	methionine-tRNA synthetase	14.2
	103402	X95404	Hs.180370	cofilin 1 (non-muscle)	4.6
	103410	X96506	Hs.295362	DR1-associated protein 1 (negative cofact	8.3
	103420	X97065	Hs.173497	Sec23 (S. cerevisiae) homolog B	4.9
	103421	X97074	Hs.119591	adaptor-related protein complex 2; sigma	5
65	103427	X97303	Hs.250655	H.sapiens mRNA for Ptg-12 protein	7
	103430	X97544	Hs.20716	translocase of inner mitochondrial membr	4.5
	103438	X98263	Hs.152720	M-phase phosphoprotein 6	4.5

	103464	Y00285	Hs.76473	Insulin-like growth factor 2 receptor	4.2
	103470	Y00796	Hs.174103	Integrin; alpha L (antigen CD11A (p180);	4.5
	103494	Y08991	Hs.83050	phosphatidylinositol 3-kinase-associated p	4.1
	103505	Y09912	Hs.33102	transcription factor AP-2 beta (activating	4.5
5	103547	Z14982	Hs.180062	proteasome (prosome; macropain) subunit	4.3
	103551	Z15115	Hs.75248	topoisomerase (DNA) II beta (180kD)	4
	103565	Z22548	Hs.146354	thioredoxin-dependent peroxide reductase	7.6
	103587	Z29083	Hs.82128	5T4 oncofetal trophoblast glycoprotein	14.6
10	103621	Z47727	Hs.150675	polymerase (RNA) II (DNA directed) pol	6.3
	103622	Z48042	Hs.278672	membrane component; chromosome 11; s	4.4
	103658	Z74615	Hs.172928	collagen; type I; alpha 1	5.9
	103680	Z93784		Homo sapiens DNA sequence from PAC	4.4
	103772	AA092473	Hs.278554	chromobox homolog 3 (Drosophila HP1 g	4.9
	103774	AA092898	Hs.92918	ESTs; Weakly similar to R07G3.8 [C. eleg	6.1
15	103821	AA157623	Hs.198793	KIAA0750 gene product	23.3
	103835	AA172215	Hs.93748	ESTs; Moderately similar to TRANSCRIP	4
	103886	AA236384	Hs.105737	ESTs; Weakly similar to gene 9306 protei	4.9
	103890	AA236843	Hs.72085	ESTs; Weakly similar to unknown [S.cere	7.8
	103892	AA243523	Hs.239189	ESTs	4.8
20	104054	AA393432	Hs.7100	hypothetical protein	5.3
	104115	AA428090	Hs.26102	ESTs	28.7
	104136	AA442669	Hs.268371	zv68f6.r1 Soares_total_fetus_Nb2HF8_9w	5.7
	104147	AA451992	Hs.283037	ESTs; Highly similar to HSPC039 protein	6.9
	104173	AA476564	Hs.76561	ESTs; Weakly similar to finger protein HZ	5.2
25	104181	AA479521	Hs.283740	ESTs	7.8
	104183	AA480838	Hs.114309	ESTs	5.1
	104192	AA486946	Hs.21321	Homo sapiens mRNA; cDNA DKFZp564	4.3
	104209	AB000221	Hs.16530	small inducible cytokine subfamily A (Cy	12.3
	104234	AB002357	Hs.168212	kinesin family member 3B	6.2
30	104271	C01687	Hs.7381	ATP synthase; H+ transporting; mitochon	4.2
	104278	C02582	Hs.109253	ESTs; Highly similar to N-terminal acetyl	4.5
	104307	D52818	Hs.111690	endosulfine alpha	4.7
	104309	D55869	Hs.284123	Homo sapiens mRNA full length insert cD	4.2
	104370	H19378	Hs.21851	Homo sapiens mRNA; cDNA DKFZp566	6.4
35	104446	L44497	Hs.7351	ESTs	4.9
	104453	M19169	Hs.123114	cystatin SN	11.6
	104476	N33807	Hs.324275	protease; serine; 15	5.6
	104558	R56678	Hs.88959	Human DNA sequence from clone 967N2	6.3
	104592	R81003	Hs.325820	serine protease; umbilical endothelium	13.6
40	104634	AA004274	Hs.19151	ESTs	6.3
	104636	AA004415	Hs.106106	ESTs	10.1
	104658	AA007145	Hs.27268	Homo sapiens mRNA; cDNA DKFZp564	4.3
	104667	AA007234	Hs.30098	ESTs	16.6
	104675	AA009596	Hs.301553	ESTs; Moderately similar to HLL ALU SU	4.6
45	104767	AA025534	Hs.8852	ESTs	4.8
	104785	AA027163	Hs.7942	ESTs	8.1
	104791	AA029046	Hs.301871	ESTs; Moderately similar to cAMP induc	10.9
	104804	AA031357	Hs.31803	ESTs; Weakly similar to N-WASP [H.sap	5.5
	104807	AA032147	Hs.23295	ESTs	10.4
50	104837	AA039469	Hs.21126	ESTs; Weakly similar to KIAA0299 [H.s	4.6
	104849	AA040270	Hs.241507	Homo sapiens mRNA; cDNA DKFZp564	4.3
	104867	AA045481	Hs.225979	Human gene from PACs 37M17 and 305B	4.5
	104884	AA053021	Hs.14511	SCO (cytochrome oxidase deficient; yeast	4.7
	104905	AA055809	Hs.26802	ESTs; Weakly similar to phosphoprotein [8.8
55	104919	AA057193	Hs.25252	ESTs	5.5
	104921	AA057839	Hs.1508	ESTs	4.2
	104926	AA058846	Hs.33363	DKFZP434N093 protein	7
	104938	AA064627	Hs.318725	ESTs; Highly similar to CGI-72 protein [H	7.1
	104943	AA065217	Hs.114218	ESTs	5.7
60	104957	AA074919	Hs.10028	ESTs; Weakly similar to ORF YJL063c [S	4.7
	104961	AA076672	Hs.33905	ESTs	5.5
	104968	AA084602	Hs.29669	ESTs	4.3
	104975	AA086071	Hs.50758	chromosome-associated polypeptide C	8.3
	104977	AA088228	Hs.18272	ESTs	6.2
65	104978	AA088458	Hs.19322	ESTs	6.7
	104987	AA101723	Hs.11861	ESTs	9.2
	105002	AA113266	Hs.182704	ESTs; Moderately similar to alternatively	6.9

	105012	AA116036	Hs.9329	chromosome 20 open reading frame 1	10.7
	105019	AA121879	Hs.9280	proteasome (prosome; macropain) subunit	5.7
	105029	AA126855	Hs.13268	ESTs	4.4
	105033	AA127984	Hs.274329	TP53 target gene 1	6.3
5	105035	AA128486	Hs.8859	ESTs	6.5
	105039	AA130349	Hs.36475	ESTs	4
	105062	AA134968	Hs.36529	ESTs	4.3
	105076	AA142858	Hs.37810	ESTs	6.4
	105087	AA147884	Hs.9812	ESTs	9.2
10	105091	AA148859	Hs.179909	ESTs; Weakly similar to IIII ALU SUBFA	5.7
	105093	AA149051	Hs.32405	ESTs	6.3
	105107	AA152302	Hs.25035	DKFZP566G223 protein	6.2
	105127	AA158132	Hs.301957	ESTs; Weakly similar to contains similar	5.7
	105132	AA159501	Hs.247280	HBV associated factor	4.2
15	105143	AA165333	Hs.24808	ESTs	4.7
	105154	AA171736	Hs.35947	methyl-CpG binding domain protein 4	9
	105162	AA176690	Hs.4084	KIAA1025 protein	9.1
	105186	AA191512	Hs.28005	Homo sapiens mRNA; cDNA DKFZp564	19.3
	105209	AA205072	Hs.227743	KIAA0980 protein	7.4
20	105223	AA211388	Hs.7750	ESTs	5.1
	105252	AA227428	Hs.9728	ESTs; Weakly similar to KIAA0512 prote	11.1
	105253	AA227448	Hs.5003	KIAA0456 protein	6.4
	105261	AA227871	Hs.6361	MEK partner 1	9.1
	105263	AA227926	Hs.6682	ESTs	6.7
25	105274	AA228122	Hs.281866	ATPase; H+ transporting; lysosomal (vacu	5.3
	105297	AA233451	Hs.183858	transcriptional intermediary factor 1	8.7
	105309	AA233790	Hs.4104	ESTs; Weakly similar to cDNA EST yk38	7.4
	105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45)	5.8
	105342	AA235286	Hs.157078	ESTs	4.5
30	105376	AA236559	Hs.8768	ESTs; Weakly similar to IIII ALU SUBFA	5.8
	105385	AA236950	Hs.8115	ESTs	5.5
	105397	AA242868	Hs.7395	ESTs; Weakly similar to house-keeping p	7.7
	105399	AA243007	Hs.16420	ESTs; Highly similar to SH3 domain-bind	5.6
	105400	AA243052	Hs.65648	RNA binding motif protein 8	5.8
35	105404	AA243303	Hs.21187	ESTs	9.1
	105409	AA243562	Hs.301855	ESTs	4.4
	105436	AA252172	Hs.237856	ESTs; Moderately similar to cAMP induc	5.1
	105483	AA255874	Hs.23458	ESTs	4.9
	105493	AA256268	Hs.10283	ESTs	6
40	105495	AA256317	Hs.28785	Homo sapiens mRNA; cDNA DKFZp586	5.2
	105496	AA256323	Hs.301997	DKFZP434N126 protein	8.7
	105500	AA256485	Hs.222399	CGI-96 protein	9.5
	105507	AA256678	Hs.226318	ESTs; Moderately similar to CCR4-associ	4.1
	105538	AA258860	Hs.32597	ring finger protein (C3H2C3 type) 6	4.1
45	105544	AA261954	Hs.24678	ESTs	8
	105546	AA262032	Hs.268281	ESTs; Weakly similar to 62D9.a [D.melan	8.1
	105549	AA262417	Hs.5415	ESTs	4.6
	105551	AA262477	Hs.25292	ribonuclease H1; large subunit	9.1
	105560	AA262783	Hs.306915	ESTs	4.5
50	105565	AA278302	Hs.18349	ESTs; Weakly similar to partial CDS [C.e	4.2
	105566	AA278323	Hs.17481	Homo sapiens clone 24606 mRNA sequen	11.9
	105575	AA278717	Hs.12772	ESTs	5.9
	105584	AA279012	Hs.3454	ESTs; Weakly similar to KIAA0665 prote	4.4
	105596	AA279418	Hs.18490	ESTs	4
55	105604	AA279787	Hs.15467	ESTs; Moderately similar to putative pho	5.6
	105610	AA279991	Hs.99872	ESTs; Weakly similar to trithorax homolo	5.3
	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564	4.8
	105627	AA281245	Hs.23317	ESTs	7.5
	105638	AA281599	Hs.247817	Homo sapiens mRNA for histone H2B	5.9
60	105645	AA282138	Hs.11325	ESTs	6.4
	105650	AA282347	Hs.25635	ESTs; Highly similar to HSPC003 [H.sap	11.3
	105666	AA283930	Hs.34905	ESTs	4.7
	105674	AA284755	Hs.279789	CDW52 antigen (CAMPATH-1 antigen)	8
	105687	AA286809	Hs.28423	ESTs	7.1
65	105700	AA287643	Hs.35254	ESTs; Weakly similar to hypothetical pro	4.9
	105705	AA290767	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434	8
	105709	AA291268	Hs.26761	DKFZP586L0724 protein	6.8

	105731	AA292711	Hs.29131	ESTs	6.4
	105753	AA298789	Hs.110857	ESTs	7
	105774	AA348014	Hs.23412	ESTs	7.1
	105784	AA350771	Hs.17850	ESTs	13.4
5	105791	AA358038	Hs.14368	SH3-binding domain glutamic acid-rich p	4.3
	105807	AA393803	Hs.16869	ESTs; Moderately similar to COLLAGEN	5.3
	105808	AA393808	Hs.286131	KIAA0438 gene product	4.1
	105812	AA394126	Hs.20814	ESTs; Highly similar to CGI-27 protein [H	14.6
	105813	AA394140	Hs.18595	ESTs	4.9
10	105819	AA397920	Hs.28783	Homo sapiens mRNA; cDNA DKFZp564	4.9
	105870	AA399623	Hs.101067	ESTs	4.8
	105874	AA400074	Hs.171118	ESTs	4
	105896	AA400999	Hs.7838	Human ring zinc-finger protein (ZNF127-	4.8
	105934	AA404248	Hs.16577	ESTs	5.2
15	105935	AA404277	Hs.263727	ESTs; Weakly similar to bisphosphate 3'-	4
	105966	AA406105	Hs.5344	adaptor-related protein complex 1; gamma	8.3
	105974	AA406321	Hs.6224	KIAA0895 protein	4.6
	105990	AA410336	Hs.29403	ESTs; Weakly similar to PROBABLE AT	4.5
	105995	AA410510	Hs.5345	ESTs	4.9
20	106000	AA410972	Hs.20726	ESTs	5.8
	106007	AA411462	Hs.11042	ESTs; Weakly similar to vcl1 [H.sapiens	6.9
	106016	AA411819	Hs.8164	KIAA0898 protein	5
	106034	AA412473	Hs.14928	ESTs	6.6
	106042	AA412700	Hs.169895	ubiquitin-conjugating enzyme E2L 6	4.6
25	106057	AA417067	Hs.289074	ESTs	4.5
	106065	AA417558	Hs.25206	ESTs	12.3
	106070	AA417761	Hs.5957	Homo sapiens clone 24416 mRNA sequen	5
	106103	AA421104	Hs.12094	ESTs	15.4
	106126	AA424006	Hs.22972	ESTs; Moderately similar to H5AR [M.m	6.4
30	106154	AA425304	Hs.6994	ESTs	5.1
	106157	AA425387	Hs.34892	ESTs	11.1
	106166	AA425872	Hs.19561	NADH dehydrogenase (ubiquinone) 1 alp	19.3
	106204	AA428024	Hs.21479	ESTs	4.7
	106210	AA428239	Hs.10338	ESTs	5.7
35	106220	AA428582	Hs.32195	ESTs; Moderately similar to metargidin p	7.7
	106236	AA429951	Hs.21104	ESTs	8
	106240	AA430074	Hs.18552	ESTs; Weakly similar to Ylr218cp [S.cere	4.4
	106263	AA431462	Hs.28329	ESTs	4.9
	106288	AA435536	Hs.24336	ESTs	8.8
40	106293	AA435591	Hs.301444	signal sequence receptor; gamma (transloc	8.7
	106310	AA436244	Hs.17240	ESTs	4.5
	106317	AA436568	Hs.108124	ESTs	4
	106328	AA436705	Hs.28020	KIAA0766 gene product	4.4
	106341	AA441798	Hs.5243	ESTs; Moderately similar to pIL2 hypoth	23.7
45	106348	AA442253	Hs.10702	ESTs	4.7
	106350	AA442763	Hs.194698	cyclin B2	6.1
	106371	AA443923	Hs.170310	ESTs	6.8
	106389	AA446949	Hs.6236	ESTs	4.7
	106394	AA447223	Hs.25320	Homo sapiens clone 25142 mRNA sequen	4.4
50	106426	AA448282	Hs.16206	ESTs; Weakly similar to F55C12.5 [C.ele	4.5
	106459	AA449741	Hs.4029	glioma-amplified sequence-41	4.8
	106462	AA449912	Hs.30532	ESTs; Highly similar to CGI-77 protein [H	5.2
	106468	AA450047	Hs.14770	ESTs	6.8
	106479	AA450351	Hs.75251	ESTs	12.4
55	106494	AA452108	Hs.18387	transcription factor AP-2 alpha (activating	4.5
	106503	AA452411	Hs.29679	ESTs; Highly similar to mediator [H.sapie	5.1
	106507	AA452584	Hs.267819	protein phosphatase 1; regulatory (inhibito	4.9
	106533	AA453786	Hs.145998	ESTs	8.3
	106568	AA455970	Hs.28285	patched related protein translocated in ren	7.6
60	106586	AA456598	Hs.57787	ESTs	8.2
	106589	AA456646	Hs.28661	ESTs	4.8
	106606	AA457730	Hs.283437	Homo sapiens clone 23851 mRNA sequen	4.4
	106611	AA458904	Hs.26267	ESTs; Weakly similar to torsinA [H.sapie	7
	106614	AA458934	Hs.256150	ESTs	4.5
65	106628	AA459857	Hs.12311	Homo sapiens clone 23570 mRNA sequen	6.5
	106637	AA459961	Hs.250824	ESTs	5.5
	106644	AA460239	Hs.12680	ESTs	4.4

	106664	AA460969	Hs.7510	mitogen-activated protein kinase kinase ki	8.4
	106698	AA463745	Hs.29403	ESTs; Weakly similar to PROBABLE AT	5.3
	106719	AA465171	Hs.236844	ESTs	5.6
5	106726	AA465339	Hs.3886	ESTs	10.1
	106747	AA476473	Hs.171957	triple functional domain (PTPRF interacti	10.4
	106759	AA477263	Hs.25584	ESTs	4.2
	106765	AA477717	Hs.306117	Interleukin 13 receptor; alpha 1	6.9
	106784	AA478558	Hs.227913	API5-like 1	5.1
10	106831	AA482014	Hs.29463	centrin; EF-hand protein; 3 (CDC31 yeast	5.1
	106836	AA482112	Hs.238707	ESTs	4.8
	106840	AA482548	Hs.5534	ESTs	10.3
	106856	AA486183	Hs.285123	ESTs; Weakly similar to similar to oxyste	6.2
	106865	AA487228	Hs.19479	ESTs	4.5
15	106878	AA488872	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586	7.9
	106888	AA489101	Hs.24734	oxysterol binding protein	6.4
	106895	AA489665	Hs.25245	ESTs	4.6
	106909	AA490323	Hs.250747	SUMO-1 activating enzyme subunit 1	4.2
	106919	AA490885	Hs.21766	ESTs	12.3
	106920	AA490899	Hs.296323	ESTs	6.2
20	106941	AA496204	Hs.237971	ESTs	4
	106942	AA496347	Hs.31314	retinoblastoma-binding protein 7	4.8
	106948	AA496788	Hs.21077	KIAA0532 protein	4
	106966	AA504631	Hs.26813	ESTs; Weakly similar to hypothetical 43.2	4.4
25	106973	AA505141	Hs.11923	Human DNA sequence from clone 167A1	5.4
	106980	AA521121	Hs.8858	bromodomain adjacent to zinc finger dom	4.1
	106981	AA521157	Hs.74101	ESTs	5.7
	106998	AA598461	Hs.195464	Insulin-like growth factor binding protein	18.7
	107008	AA598710	Hs.23740	ESTs	6.2
	107028	AA599214	Hs.24143	ESTs	4.1
30	107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta	5.3
	107052	AA600134	Hs.12482	glyceronephosphate O-acyltransferase	4.8
	107053	AA600147	Hs.5741	ESTs; Weakly similar to NADH-cytochro	5.8
	107056	AA600310	Hs.18720	programmed cell death 8 (apoptosis-induc	4.9
	107080	AA609210	Hs.19221	ESTs	8.4
35	107102	AA609723	Hs.30852	ESTs	8
	107109	AA609943	Hs.32793	ESTs	9.5
	107129	AA620553	Hs.4756	flap structure-specific endonuclease 1	4.9
	107132	AA620598	Hs.9052	ESTs	5.3
	107136	AA620795	Hs.8207	ESTs	4
40	107140	AA620889	Hs.170088	ESTs	6.7
	107151	AA621169	Hs.8687	ESTs	19
	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [8.1
	107174	AA621714	Hs.25338	ESTs	8.5
45	107217	D51095	Hs.35861	DKFZP586E1621 protein	7.2
	107252	D59971	Hs.25925	ESTs	7.9
	107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine;po	5.6
	107299	T40327	Hs.30661	lung resistance-related protein	8.4
	107324	T81665	Hs.278422	DKFZP586G1122 protein	7.5
50	107372	U85625	Hs.8297	ribonuclease 6 precursor	4.7
	107373	U85773	Hs.154695	phosphomannomutase 2	4.8
	107481	W58247	Hs.279766	Homo sapiens kinesin superfamily motor	6.3
	107531	Y13936	Hs.17883	protein phosphatase 1G (formerly 2C); ma	8.3
	107859	AA024835	Hs.47684	potassium voltage-gated channel; delayed	7.3
55	107860	AA026030	Hs.61311	ESTs; Weakly similar to CALPAIN 2; LA	7.3
	107908	AA026894	Hs.42826	ESTs	4.9
	108039	AA041341	Hs.46670	ESTs	5.4
	108040	AA041551	Hs.159971	ESTs	8.4
	108102	AA046424	Hs.49433	ESTs; Weakly similar to HYPOTHETICA	6.6
	108217	AA058686	Hs.62588	ESTs	7.7
60	108255	AA063157	Hs.172608	ESTs	4
	108358	AA071514	Hs.1634	ESTs	4
	108609	AA100694	Hs.69499	Human DNA sequence from BAC 15E1 o	5.5
	108647	AA112396	Hs.44276	ESTs; Moderately similar to HOMEBO	14.3
	108676	AA115562	Hs.274417	Homo sapiens mRNA; cDNA DKFZp564	5.2
65	108687	AA120785	Hs.54347	ESTs	5.6
	108695	AA121315	Hs.70823	KIAA1077 protein	10.5
	108733	AA126422		zn84f1.s1 Stratagene lung carcinoma 9372	4.4

	108774	AA128125	Hs.71040	ESTs; Moderately similar to CELL GROW	4.6
	108828	AA131584	Hs.273344	DKFZP584O0463 protein	5.5
	108872	AA134063	Hs.111680	ESTs	7.2
	108884	AA134958	Hs.293591	ESTs	11.3
5	108893	AA135894	Hs.194891	retinoic acid induced 3	8.9
	109008	AA156360	Hs.87128	ESTs	14.7
	109010	AA156460	Hs.44229	dual specificity phosphatase 12	4.9
	109011	AA156542	Hs.72127	ESTs	4.6
	109042	AA159525	Hs.71779	Homo sapiens DNA from chromosome 19	7.2
10	109086	AA166695	Hs.270737	tumor necrosis factor (ligand) superfamily	4
	109090	AA167006	Hs.70499	ESTs	5.9
	109101	AA167708	Hs.52184	ESTs	4.2
	109112	AA169379	Hs.257924	ESTs	4
	109160	AA179387	Hs.301997	DKFZP434N126 protein	4
15	109166	AA179845	Hs.73625	RAB6 Interacting; kinesin-like (rakkinesin	13.6
	109178	AA181600	Hs.283707	ESTs	11.8
	109179	AA181902	Hs.192789	ESTs; Weakly similar to III ALU SUBFA	5.4
	109261	AA195255	Hs.61779	ESTs	6.7
	109270	AA195515	Hs.3585	ESTs; Weakly similar to alternatively spliced	4.9
20	109277	AA196332	Hs.86043	ESTs	5.4
	109313	AA206800	Hs.86276	ESTs; Moderately similar to zinc finger p	5.5
	109415	AA227219	Hs.110826	trinucleotide repeat containing 9	20.1
	109454	AA232255	Hs.295232	ESTs	4.7
	109467	AA232904	Hs.83187	ESTs	6.8
25	109481	AA233342	Hs.289069	ESTs; Weakly similar to WD40 protein C	10.6
	109508	AA233892	Hs.55902	ESTs; Weakly similar to III ALU SUBFA	8
	109514	AA234087	Hs.262346	ESTs; Weakly similar to CRF2: function	8.2
	109572	F02027	Hs.171937	ESTs	4.8
	109632	F04165	Hs.235873	ESTs; Weakly similar to K11C4.2 [C.eleg	5.2
30	109644	F04477	Hs.291531	ESTs; Moderately similar to GLYCERAL	6.6
	109703	F09684	Hs.24792	ESTs; Weakly similar to ORF YOR283w	7.1
	109726	F10009	Hs.9196	ESTs	5
	109747	F10161	Hs.22969	ESTs	4.7
	109799	F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA	4.5
35	109814	F10979	Hs.153106	Homo sapiens clone 23728 mRNA sequen	8.7
	110189	H20543	Hs.6278	DKFZP586B1621 protein	16.6
	110240	H25577	Hs.176588	ESTs; Weakly similar to CYTOCHROME	6.2
	110280	H29285	Hs.32468	ESTs	4.5
40	110520	H56965	Hs.4082	y09f06.s1 Soares fetal liver spleen 1NFL	5.7
	110561	H59617	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CO	19.5
	110707	H95079	Hs.15617	ESTs; Weakly similar to III ALU SUBFA	6.2
	110734	H98714	Hs.24131	ESTs	30.2
	110770	N22262	Hs.131705	ESTs	5.8
	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino aci	8.2
45	110787	N24716	Hs.12244	ESTs; Weakly similar to C44B9.1 [C.eleg	6.7
	110794	N25262	Hs.27931	ESTs	5.9
	110799	N26101	Hs.323401	Human ring zinc-finger protein (ZNF127-	4
	110818	N29454	Hs.27552	ESTs; Weakly similar to putative p150 [H	4.3
	110839	N30856	Hs.30246	solute carrier family 19 (thiamine transpo	12.8
50	110844	N31952	Hs.167531	Homo sapiens mRNA full length insert cD	10.1
	110854	N32919	Hs.27931	ESTs	4.7
	110856	N33053		ESTs; Weakly similar to S164 [H.sapiens	4.2
	110860	N33438	Hs.170065	ESTs	12.5
	110897	N39148	Hs.6880	DKFZP434D156 protein	4
55	110915	N46252	Hs.29724	ESTs	23.2
	110935	N48787	Hs.305979	protease inhibitor 1 (anti-elastase); alpha-	4.8
	110970	N51374	Hs.96870	Homo sapiens mRNA full length insert cD	5.4
	111006	N53375	Hs.166146	Homer; neuronal immediate early gene; 3	4.7
	111008	N53388	Hs.7222	ESTs	13.3
60	111018	N54067	Hs.3628	mitogen-activated protein kinase kinase ki	5.7
	111084	N59543	Hs.15456	PDZ domain containing 1	8.3
	111100	N62522	Hs.20450	ESTs	14.3
	111125	N63823	Hs.269115	ESTs	7.9
	111132	N64378	Hs.83293	ESTs; Highly similar to unknown function	4.4
65	111139	N64683	Hs.290943	ESTs	6
	111164	N66857	Hs.14808	ESTs; Weakly similar to III ALU CLASS	4.1
	111172	N67102	Hs.21851	Homo sapiens mRNA; cDNA DKFZp586	5.5

	111178	N67227	Hs.24633	ESTs	5.7
	111179	N67239	Hs.10760	ESTs	37
	111181	N67278	Hs.171802	ESTs; Weakly similar to hypothetical pro	5.6
5	111184	N67437	Hs.243901	Homo sapiens mRNA; cDNA DKFZp564	8.7
	111221	N68869	Hs.15119	ESTs	7.3
	111223	N68921	Hs.297939	ESTs; Weakly similar to neogenin (H.sap	9
	111229	N69113	Hs.110855	ESTs	8.9
	111241	N69514	Hs.288880	ESTs; Weakly similar to CGI-82 protein [6.9
10	111268	N70481	Hs.26118	Homo sapiens clone 24766 mRNA sequen	4.5
	111295	N73275	Hs.21275	ESTs; Weakly similar to ubiquitin-conjug	5.6
	111299	N73808	Hs.24936	ESTs	8.5
	111336	N79565	Hs.29894	ESTs	6.7
	111357	N91023	Hs.87128	ESTs	15
15	111370	N92915	Hs.94631	brefeldin A-inhibited guanine nucleotide-e	5.2
	111806	R33468	Hs.279008	ESTs	10
	111825	R35885	Hs.286148	stromal antigen 1	4.5
	111836	R36228	Hs.25119	ESTs	7.2
	111890	R38678	Hs.12365	ESTs	17.3
20	111923	R39995	Hs.25925	Homo sapiens clone 23860 mRNA sequen	7.3
	111942	R40576	Hs.21590	ESTs	9.2
	111987	R42036	Hs.6763	KIAA0942 protein	10.6
	112101	R44793	Hs.296341	adenylyl cyclase-associated protein 2	5.3
	112134	R46025	Hs.7413	ESTs	17.4
25	112197	R49482	Hs.5637	ESTs	4.4
	112244	R51309	Hs.70823	KIAA1077 protein	11
	112253	R51818		Homo sapiens mRNA; cDNA DKFZp566	9.3
	112305	R54822	Hs.26244	ESTs	4.4
	112449	R63802	Hs.124186	ring finger protein 2	6.3
30	112483	R66534	Hs.285885	ESTs	4.9
	112519	R68631	Hs.11861	ESTs	14.3
	112610	R79392	Hs.23643	ESTs	5.2
	112693	R88741	Hs.91065	ESTs; Moderately similar to proliferation	4.6
	112751	R93597	Hs.8207	ESTs	5.6
35	112801	R97486	Hs.157160	protein kinase; DNA-activated; catalytic p	8.7
	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	5.9
	112871	T03352	Hs.12285	ESTs	5.8
	112908	T10065	Hs.3530	TLS-associated serine-arginine protein	4.1
	112966	T17119	Hs.102548	glucocorticoid receptor DNA binding fact	5.7
40	112971	T17185	Hs.83883	ESTs	6.4
	112995	T23528	Hs.7155	ESTs; Weakly similar to TYK1 protein [M	9.1
	113047	T25867	Hs.7549	ESTs	5.4
	113075	T34660	Hs.6986	ESTs; Weakly similar to IIII ALU SUBFA	5.7
	113117	T47819	Hs.159153	ESTs	5.8
45	113206	T58044	Hs.241471	ESTs; Moderately similar to IIII ALU SU	6.4
	113248	T63857		yc16e1.s1 Stratagene lung (#93721) Homo	4.6
	113260	T64896	Hs.287420	ESTs	6.9
	113277	T65797	Hs.11774	protein (peptidyl-prolyl cis/trans isomeras	5.6
	113278	T65802	Hs.11135	yc11h10.s1 Stratagene lung (#937210) Ho	4.5
	113440	T86121	Hs.191445	ESTs	6.4
50	113523	T90037	Hs.95549	ESTs	6.4
	113604	T92735	Hs.296083	ESTs	8.7
	113702	T97307		ESTs; Moderately similar to IIII ALU SU	9.5
	113793	W19222	Hs.7041	ESTs; Weakly similar to IIII ALU SUBFA	5.2
55	113794	W37382	Hs.11090	ESTs	11.9
	113808	W44735	Hs.9286	ESTs	16.7
	113811	W44928	Hs.6994	ESTs	4
	113822	W47350	Hs.17466	retinoic acid receptor responder (tazaroten	4.8
	113823	W47388	Hs.55099	rab6 GTPase activating protein (GAP and	4
60	113836	W56792	Hs.12040	ESTs; Weakly similar to KIAA0881 prote	4.1
	113857	W65477	Hs.5297	Homo sapiens mRNA; cDNA DKFZp564	4.3
	113886	W72471	Hs.23920	ESTs	4.6
	113895	W73738	Hs.12921	ESTs	7.1
	113923	W80763	Hs.3849	ESTs; Weakly similar to FK506-binding p	6.8
	113931	W81205	Hs.3496	ESTs	6.1
65	113950	W85765	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434	14
	113970	W86748	Hs.8109	ESTs	15
	114051	W94942	Hs.177534	dual specificity phosphatase 10	5.4

	114057	W96222	Hs.34192	ESTs	4.8
	114086	Z38266	Hs.288649	Homo sapiens PAC clone DJ0777023 fro	5.1
	114098	Z38347	Hs.118338	ESTs; Weakly similar to similar to S. cere	6.2
	114109	Z38435	Hs.184108	ribosomal protein L21	4.6
5	114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0886 prote	22
	114138	Z38763	Hs.15740	amyloid beta (A4) precursor protein-bind	8.8
	114149	Z38814	Hs.27196	ESTs	4
	114162	Z38909	Hs.22265	ESTs	7.2
	114177	Z39062	Hs.23740	ESTs	5.3
10	114196	Z39211	Hs.150926	fucose-1-phosphate guanylyltransferase	4.4
	114208	Z39301	Hs.7859	ESTs	5.1
	114250	Z39897	Hs.13297	ESTs	7.2
	114251	Z39898	Hs.21948	ESTs	14.7
	114292	Z40715	Hs.184641	delta-6 fatty acid desaturase	19.4
15	114297	Z40758	Hs.173091	DKFZP434K151 protein	8.9
	114334	Z41342	Hs.22941	ESTs	13.7
	114460	AA024804	Hs.26102	ESTs	10.1
	114471	AA028074	Hs.104613	ESTs	5.7
	114480	AA032243	Hs.151678	UDP-N-acetyl-alpha-D-galactosamine:po	7.3
20	114518	AA046407	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like 1	4.3
	114542	AA055769	Hs.293380	ESTs	11.7
	114549	AA056484	Hs.292833	ESTs	7.3
	114652	AA101416	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIAT	6.1
	114673	AA113303	Hs.95583	transmembrane 4 superfamily member (te	4.3
25	114698	AA126951	Hs.110857	ESTs; Highly similar to putative DNA-dir	7.1
	114767	AA146885	Hs.154443	minichromosome maintenance deficient (S	5.3
	114799	AA159323	Hs.109929	ESTs	4.2
	114804	AA160363	Hs.269956	ESTs	4.8
	114811	AA161161	Hs.95907	multiple inositol polyphosphate phosphat	7.1
30	114821	AA165313	Hs.55468	ESTs	4.4
	114852	AA235035	Hs.38260	ESTs; Moderately similar to ubiquitin spe	5
	114901	AA236276	Hs.196437	ESTs; Weakly similar to R28660_1; parli	16.9
	114902	AA236359	Hs.39504	ESTs	5.1
	114940	AA243012	Hs.75928	ESTs	8.5
35	114965	AA250737	Hs.72472	ESTs	35.1
	115047	AA252627	Hs.82916	homeo box B5	5.7
	115054	AA252863	Hs.87729	ESTs	6.2
	115061	AA253217	Hs.41271	ESTs	13
	115082	AA255557	Hs.198269	NADH dehydrogenase (ubiquinone) 1 alp	28.2
40	115116	AA256486	Hs.62275	ESTs	8.8
	115140	AA256030	Hs.279938	ESTs; Weakly similar to supported by GE	4.1
	115205	AA262470	Hs.284216	ESTs	8.3
	115206	AA262491	Hs.186572	ESTs	5.1
	115239	AA278650	Hs.73291	ESTs; Weakly similar to similar to the bet	4.6
45	115242	AA278755	Hs.283732	ESTs	8.3
	115249	AA278961	Hs.71124	ESTs	10.1
	115259	AA279071	Hs.13453	splicing factor 3b; subunit 1; 155kD	9.5
	115285	AA279799	Hs.293736	ESTs	5.8
	115291	AA279943	Hs.122579	ESTs	5.1
50	115357	AA281793	Hs.72988	ESTs	5
	115377	AA282247	Hs.193063	ESTs	6.1
	115400	AA283198	Hs.89113	ESTs	4.9
	115439	AA284561	Hs.193090	ESTs	5.8
	115471	AA287138	Hs.59346	ESTs; Weakly similar to ASPARTYL-TR	11.7
55	115506	AA292537	Hs.45207	Human DNA sequence from clone 620E1	6.8
	115522	AA331393	Hs.47378	ESTs	5.8
	115572	AA398392	Hs.59594	ESTs; Weakly similar to F33G12.3 gene p	9.7
	115587	AA399264	Hs.283037	ESTs; Highly similar to HSPC039 protein	8.7
	115600	AA400247	Hs.42173	ESTs	4
60	115612	AA400948	Hs.71243	ESTs; Weakly similar to zinc finger prote	8.4
	115646	AA404352	Hs.305971	ESTs	5.3
	115652	AA405098	Hs.38178	ESTs	16.1
	115657	AA405620	Hs.55158	ESTs; Weakly similar to weak similarity t	4.7
	115658	AA405625	Hs.183056	Human DNA sequence from clone 34B21	5.1
65	115675	AA406546	Hs.82065	Homo sapiens mRNA; cDNA DKFZp564	20.5
	115721	AA417102	Hs.90960	ESTs	4.8
	115763	AA421560		ESTs	7

	115764	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) homo	41.6
	115835	AA428576	Hs.41371	ESTs	4.2
	115844	AA430124	Hs.7773	ESTs	11.9
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity	33.5
5	115888	AA435839	Hs.76591	KIAA0887 protein	7.2
	115922	AA441911	Hs.71869	ESTs; Weakly similar to KIAA0926 prote	5.1
	115941	AA443602	Hs.46679	ESTs	4.8
	115947	AA443793	Hs.94761	ESTs	8.3
	115948	AA443798	Hs.43445	poly(A)-specific ribonuclease (deadenyat	13.5
10	115951	AA443918	Hs.301048	cofilin 1 (non-muscle)	7.5
	115967	AA446887	Hs.42911	ESTs	8.8
	115984	AA447687	Hs.91109	ESTs	13.1
	116009	AA449448	Hs.44238	ESTs	5.5
	116024	AA451748	Hs.83883	Human DNA sequence from clone 718J7	7.5
15	116028	AA452112	Hs.42644	thioredoxin-like	12.7
	116050	AA453656	Hs.88417	ESTs	7.2
	116097	AA456099	Hs.176376	ESTs	11.8
	116108	AA457566	Hs.28777	ESTs	4.5
	116121	AA459254	Hs.48855	ESTs	4.5
20	116127	AA459703	Hs.279884	v-myc avian myelocytomatosis viral onco	4.3
	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonucle	7.6
	116142	AA460649	Hs.39457	ESTs	4.8
	116204	AA465701	Hs.108646	ESTs	6.8
	116221	AA478397	Hs.50180	ESTs	4.9
25	116222	AA478415	Hs.89966	ESTs	4
	116238	AA479362	Hs.47144	DKFZP586N0819 protein	4.6
	116246	AA479961	Hs.250646	ESTs; Highly similar to ubiquitin-conjuga	4
	116249	AA480886	Hs.86693	ESTs	18.5
	116250	AA480975	Hs.44829	ESTs	10.8
30	116254	AA481146	Hs.41086	ESTs; Weakly similar to OXYSTEROL-B	9.1
	116255	AA481256	Hs.88201	ESTs; Weakly similar to lysophospholipa	8.4
	116254	AA482594	Hs.272239	Homo sapiens mRNA; cDNA DKFZp586	7.2
	116265	AA482595	Hs.55189	ESTs; Weakly similar to F25B5.3 [C.eleg	11.1
	116282	AA486560	Hs.204501	ESTs; Weakly similar to Wiskott-Aldrich	6.2
35	116298	AA489046	Hs.94109	ESTs	4.9
	116300	AA489194	Hs.159471	ESTs; Weakly similar to snRNP protein B	4.6
	116327	AA490959	Hs.28005	Homo sapiens mRNA; cDNA DKFZp554	5.8
	116334	AA491457	Hs.48948	ESTs	4.3
	116337	AA496127	Hs.44070	ESTs	8.4
40	116351	AA504116	Hs.82501	Homo sapiens mRNA; cDNA DKFZp434	5.3
	116357	AA504806	Hs.90797	Homo sapiens clone 23620 mRNA sequen	5.2
	116415	AA609204	Hs.27973	KIAA0874 protein	8.6
	116443	AA620313	Hs.190488	ESTs; Weakly similar to KERATIN; TYP	4.5
	116470	C13992	Hs.83484	ESTs	4.5
45	116480	C14088		glyceraldehyde-3-phosphate dehydrogena	5.6
	116578	D51272	Hs.75337	nucleolar phosphoprotein p130	4.1
	116579	D51276	Hs.81915	leukemia-associated phosphoprotein p18	5.8
	116626	F02028	Hs.81907	ESTs	4.9
	116647	F03069	Hs.15395	ESTs; Weakly similar to ARGINYL-TRN	6.1
50	116674	F04816	Hs.92127	ESTs	10.6
	116680	F06613	Hs.273829	LINE retrotransposable element 1	4.2
	116700	F09983	Hs.317589	ESTs	13
	116724	F13665	Hs.66641	ESTs	8.5
	116726	F13681	Hs.53913	ESTs	5.6
55	116732	F13779	Hs.165909	ESTs	11.6
	116734	F13789	Hs.93796	DKFZP586D2223 protein	5.4
	116760	H11054	Hs.155342	protein kinase C; delta	4.3
	116780	H22566	Hs.30098	ESTs	5.7
	116786	H25836	Hs.301527	tumor necrosis factor (ligand) superfamily	8.8
60	116787	H28581	Hs.15841	ESTs	8.6
	116790	H29532	Hs.101174	microtubule-associated protein tau	22.2
	116803	H47357	Hs.109701	ESTs; Moderately similar to weak similar	6.7
	116877	H68116	Hs.168732	ESTs	6.5
	116921	H72948	Hs.821	biglycan	20.7
65	117216	N20083	Hs.42792	ESTs	4.4
	117232	N20579	Hs.61153	ESTs	7.4
	117284	N22162	Hs.183779	ESTs; Weakly similar to cDNA EST yk33	4.1

	117344	N24046	Hs.210706	ESTs	7.4
	117367	N24954	Hs.42502	ESTs	10.5
	117392	N26175	Hs.93405	ESTs	5.8
	117394	N26257	Hs.39871	KIAA0727 protein	8.4
5	117412	N26722	Hs.42645	ESTs	18.1
	117498	N31726	Hs.44268	ESTs; Highly similar to myelin gene expr	5.8
	117557	N33920	Hs.44532	diubiquitin	12.3
	117634	N36421	Hs.13323	ESTs; Weakly similar to SODIUM- AND	4.4
	117639	N36923	Hs.44833	ESTs	6
10	117754	N47469	Hs.59757	ESTs	7.6
	117852	N49408	Hs.136102	KIAA0853 protein	5.9
	117879	N50050	Hs.303025	ESTs; Weakly similar to keratin; 67K typ	7.9
	117924	N51056	Hs.38891	ESTs	7.9
	117950	N51394	Hs.75478	KIAA0956 protein	5
15	117992	N52000	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586	7
	118138	N57773	Hs.93560	ESTs; Weakly similar to trig [R.norvegicu	4.8
	118215	N62195	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A	13.4
	118229	N62339	Hs.166254	heat shock 90kD protein 1; alpha	5.4
	118265	N62827	Hs.48645	EST	4.2
20	118336	N63604	Hs.47166	ESTs	7.2
	118363	N64168	Hs.48938	ESTs	6
	118429	N66158	Hs.74649	ESTs	4.1
	118470	N66769	Hs.291033	ESTs	5.4
	118472	N66818	Hs.42179	ESTs	10.8
25	118475	N66845		ESTs; Weakly similar to III ALU CLASS	4.5
	118493	N67149	Hs.50115	ESTs	5.3
	118528	N67889	Hs.49397	ESTs	10.4
	118542	N68010	Hs.49427	ESTs	7.9
	118600	N69222		ESTs	9.2
30	118695	N71781	Hs.50081	Homo sapiens mRNA full length insert cD	9.8
	118698	N72113	Hs.50187	ESTs	4.3
	118901	N90719	Hs.94445	ESTs	8.1
	118952	N92966		ESTs; Highly similar to CGI-90 protein [H	12.5
	118976	N93629	Hs.93391	ESTs	5
35	118986	N94362	Hs.125830	ESTs	7.3
	118989	N94439	Hs.45105	ESTs	8.2
	119027	N99256	Hs.114611	ESTs	5
	119042	R05316	Hs.5472	ESTs	4
	119075	R36451	Hs.287820	fibronectin 1	6
40	119260	T15916	Hs.102950	ESTs; Highly similar to coat protein gamm	4.1
	119271	T16387	Hs.65328	ESTs	12.1
	119298	T23820	Hs.155478	cyclin T2	5.6
	119302	T25725		ESTs	14.3
	119341	T62571	Hs.146388	microtubule-associated protein 7	4
45	119495	W35390	Hs.55533	ESTs	5.3
	119580	W42451	Hs.92260	high-mobility group protein 2-like 1	5.6
	119602	W46286	Hs.233694	ESTs; Weakly similar to ZK1058.5 [C.ele	6.5
	119620	W47620	Hs.56009	2'-5'-oligoadenylate synthetase 3	8.1
	119676	W60473	Hs.57787	ESTs	5.5
50	119717	W69134	Hs.57987	ESTs	4.6
	119729	W69747	Hs.94806	KIAA1062 protein	4
	119805	W73788	Hs.43213	ESTs	4
	119859	W80702	Hs.58461	ESTs	4.8
	119867	W80852	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic re	4.2
55	119873	W81129	Hs.44865	Homo sapiens mRNA; cDNA DKFZp586	4.8
	119899	W84767	Hs.58698	ESTs	5.9
	119940	W86779	Hs.272531	DKFZP586B0319 protein	9
	119943	W86835	Hs.14158	copline III	4.8
	119970	W87812	Hs.93581	Homo sapiens mRNA; cDNA DKFZp586	4
60	120131	Z38656	Hs.75887	coatomer protein complex; subunit alpha	4.2
	120150	Z39549	Hs.153746	ESTs	11
	120206	Z40805	Hs.91668	ESTs	8.2
	120241	Z41815	Hs.65946	ESTs	15.6
	120255	AA169752	Hs.5672	ESTs; Weakly similar to Similarity to Yea	4.2
65	120314	AA194186	Hs.221040	KIAA1038 protein	6.8
	120325	AA196651	Hs.104108	ESTs	15.2
	120352	AA211400	Hs.193172	ESTs	6.8

	120428	AA236822	Hs.173694	KIAA1097 protein	5.6
	120524	AA261852	Hs.192905	ESTs	5.6
	120528	AA262107	Hs.104413	ESTs	4.5
5	120571	AA280738	Hs.34892	ESTs	4.9
	120649	AA287115	Hs.192843	ESTs	4.5
	120655	AA287347	Hs.238205	ESTs	6.7
	120668	AA287833	Hs.292913	ESTs	8.3
	120712	AA292654	Hs.102506	eukaryotic translation initiation factor 2 al	4.6
10	120713	AA292655	Hs.96557	ESTs	10.6
	120724	AA293470	Hs.100747	ESTs	5.4
	120873	AA358015		EST	7.1
	120885	AA365515	Hs.301872	ESTs; Moderately similar to IIII ALU SU	4.6
	120919	AA381125	Hs.301444	ESTs	8.2
15	120948	AA397822	Hs.104650	ESTs; Highly similar to similar to mago n	8.6
	120969	AA398116	Hs.129206	casein kinase 1; gamma 3	10.5
	120977	AA398155	Hs.97600	ESTs	10.9
	121103	AA398936	Hs.97697	EST	7.4
	121291	AA401753	Hs.8186	lung cancer candidate	5.3
20	121320	AA403008	Hs.301927	T-cell receptor; alpha (V;D;J;C)	13.5
	121463	AA411745	Hs.239681	ESTs; Weakly similar to KIAA0554 prote	8.9
	121596	AA416740	Hs.174104	ESTs	22.6
	121723	AA419622	Hs.104800	ESTs; Weakly similar to Mouse 19.5 mRN	8
	121748	AA421171	Hs.234545	ESTs	5.6
25	122125	AA434411	Hs.98806	ESTs	5.3
	122522	AA449444	Hs.98969	ESTs	4
	122655	AA454756	Hs.97837	ESTs	4
	122704	AA456326	Hs.99445	ESTs	6.2
	122782	AA459894	Hs.99472	ESTs	5.3
30	122856	AA463740	Hs.75367	Src-like-adaptor	13.1
	122882	AA465381	Hs.108812	ESTs; Weakly similar to B0041.5 [C.eleg	5.5
	122928	AA476578	Hs.101840	ESTs	8.3
	122974	AA478625	Hs.194215	ESTs	6
	122997	AA479295	Hs.105290	Kelch motif containing protein	12.5
35	123016	AA480103	Hs.323231	ESTs; Weakly similar to alternatively spl	4.4
	123107	AA486071	Hs.104207	ESTs	8.3
	123111	AA486273	Hs.191721	ESTs	4.2
	123114	AA486407	Hs.129928	ESTs; Moderately similar to KIAA0454 p	5.2
	123136	AA487449	Hs.194024	ESTs	4.2
40	123137	AA487468	Hs.100686	ESTs; Weakly similar to secreted cement	14.6
	123169	AA488892		ESTs; Weakly similar to Gag-Pol polypro	4.5
	123176	AA489020	Hs.69233	ESTs	5.2
	123338	AA504249	Hs.187585	ESTs	4
	123436	AA598714	Hs.223014	protease; serine; 15	7.3
45	123442	AA598803	Hs.111496	ESTs	5.9
	123449	AA598899	Hs.112493	Homo sapiens mRNA; cDNA DKFZp564	4.1
	123494	AA599786	Hs.112110	ESTs	4
	123503	AA600121	Hs.293156	ESTs	12.8
	123533	AA608751		ESTs; Weakly similar to IIII ALU SUBFA	7.9
50	123619	AA609200		ESTs	23.1
	123673	AA609471	Hs.158549	ESTs	6.6
	123729	AA609778	Hs.278672	membrane component; chromosome 11; s	4.7
	123819	AA620636	Hs.112264	ESTs	4
	123960	AA621785	Hs.287733	methylmalonate-semialdehyde dehydroge	7.8
55	124000	D57317	Hs.74861	activated RNA polymerase II transcription	4.4
	124006	D60302	Hs.270016	ESTs	20.6
	124012	D80240	Hs.241471	HUM5G11A Human fetal brain (TFujiwa	6.7
	124021	F02859	Hs.13974	ESTs	4.7
	124049	F10523	Hs.74519	primase; polypeptide 2A (58kd)	4.7
	124059	F13673	Hs.283713	ESTs	7.7
60	124243	H66710	Hs.133525	ESTs	5.5
	124308	H93575	Hs.241507	Homo sapiens mRNA; cDNA DKFZp564	11.4
	124314	H94877	Hs.215766	GTP-binding protein	13.7
	124315	H94892	Hs.288757	v-ral simian leukemia vral oncogene hom	14
	124350	N21359	Hs.101282	Homo sapiens mRNA; cDNA DKFZp434	8.6
65	124352	N21626	Hs.102406	ESTs	7.2
	124357	N22401		yw37g07.s1 Morton Fetal Cochlea Homo	5.2
	124390	N29325	Hs.7535	ESTs; Highly similar to COBW-like place	7.9

	124438	N40188	Hs.11090	ESTs	9.5
	124447	N48000		Homo sapiens mRNA; cDNA DKFZp586	4.8
	124457	N50114	Hs.266175	ESTs	6.1
5	124539	N63172	Hs.146409	cell division cycle 42 (GTP-binding prote	5.6
	124626	N74604	Hs.11090	ESTs	12.8
	124632	N79515	Hs.306117	interleukin 13 receptor; alpha 1	6.4
	124644	N91279	Hs.109654	ESTs; Moderately similar to outer membr	8.3
	124676	R01037	Hs.181013	phosphoglycerate mutase 1 (brain)	12.3
	124677	R01073		ESTs; Weakly similar to !!!!! ALU CLASS	5.4
10	124724	R12405	Hs.112423	Homo sapiens mRNA; cDNA DKFZp586	6.6
	124773	R40923	Hs.106604	ESTs	4.9
	124777	R41933		ESTs	7.2
	124792	R44357	Hs.48712	ESTs; Weakly similar to cDNA EST EMB	8.6
	124857	R63652	Hs.137190	ESTs	4.9
15	124911	R88992	Hs.180612	ESTs	4.7
	124955	T10598	Hs.324841	ESTs; Weakly similar to !!!!! ALU SUBFA	4.4
	124958	T11134	Hs.431	murine leukemia viral (bmi-1) oncogene h	12.6
	125038	T78089	Hs.270134	ESTs	4.1
	125092	T92544	Hs.137548	CD84 antigen (leukocyte antigen)	14.8
20	125132	W15495	Hs.129781	chromosome 21 open reading frame 5	6.7
	125144	W37999	Hs.24336	ESTs	4.8
	125154	W38419		ESTs	5.3
	125243	W86423	Hs.105413	ESTs	6.6
25	125279	W93640	Hs.4779	ESTs; Moderately similar to similar to AD	5.8
	125299	Z39436	Hs.102720	ESTs	12.2
	125303	Z39821	Hs.288193	ESTs	10.2
	125304	Z39833	Hs.124940	GTP-binding protein	6.8
	125474	AA151216	Hs.75103	tyrosine 3-monooxygenase/tryptophan 5-m	8
	125509	AA044232	Hs.288987	ESTs	5.4
30	125580	AA126504	Hs.267812	sorting nexin 4	4.1
	125582	AA597383	Hs.74649	cytochrome c oxidase subunit VIc	11.5
	125670	AI432621	Hs.82685	CD47 antigen (Rh-related antigen; integri	4
	125698	AA748483	Hs.191356	general transcription factor IIf; polypeptl	9.4
	125745	AI283493	Hs.75722	ribophorin II	6.2
35	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564	25.9
	125972	AA434562	Hs.35406	ESTs	4.1
	126160	N90960	Hs.265398	ESTs; Weakly similar to transformation-r	16.4
	126257	N99638	Hs.124084	tumor necrosis factor receptor superfamily	9.5
	126337	AI066486	Hs.40500	similar to S. cerevisiae RER1	5.6
40	126405	U46278	Hs.122489	ESTs	7.5
	126537	W40262	Hs.146310	ESTs; Weakly similar to putative p150 [H	4.1
	126590	W78968	Hs.181307	H3 histone; family 3A	4.5
	126712	AA205862	Hs.7942	ESTs	5.2
45	126721	T72569	Hs.125359	Thy-1 cell surface antigen	4.4
	126764	AI334393	Hs.102178	ESTs	4.6
	126804	AI203334	Hs.160628	ESTs	11.7
	126819	AA305536	Hs.279607	ESTs	4
	126877	AI052047	Hs.26102	ESTs	7
50	126991	R31652	Hs.821	biglycan	5.6
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmidl metaph	14.3
	127514	AA826926	Hs.204214	ESTs	4.5
	127663	W07286	Hs.10340	ESTs; Weakly similar to weak similarity t	5.1
	127677	AA916752	Hs.264190	ESTs; Highly similar to MEM3 [M.muscu	17.3
55	127814	AA761755	Hs.136713	ESTs; Weakly similar to V4-1 [H.sapiens	4.1
	127997	AI281549	Hs.311054	ESTs	5.5
	128092	AA904617	Hs.166229	ESTs	5.8
	128218	H02682	Hs.292154	ESTs; Moderately similar to recombinatio	5.8
	128465	D59653	Hs.241471	EST	7.4
	128482	U83908	Hs.296251	programmed cell death 4	5.8
60	128517	AA280617	Hs.100861	ESTs; Weakly similar to p60 katanin [H.s	8.3
	128530	AA504343	Hs.183475	Homo sapiens clone 25061 mRNA sequen	6.6
	128559	AA228801	Hs.101448	metastasis associated 1	5.2
	128574	AA412048	Hs.38260	keratin 8	5.1
65	128595	U31875	Hs.152677	short-chain alcohol dehydrogenase family	27.1
	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecule	13.2
	128629	AA399187	Hs.102708	DKFZP434A043 protein	6.7
	128649	AA142853	Hs.103106	Homo sapiens mRNA for G7b protein [G	4.5

	128651	AA446990	Hs.103135	ESTs	6.1
	128653	R48943	Hs.10315	solute carrier family 7 (cationic amino aci	4.4
	128656	AA458542	Hs.10326	coatamer protein complex; subunit epsilon	14.3
5	128717	T30617	Hs.104222	Homo sapiens mRNA; cDNA DKFZp586	24.5
	128727	M64174	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	7.3
	128764	N49308	Hs.104938	ESTs; Weakly similar to alpha 1(XVIII) c	9.2
	128781	X85372	Hs.105465	small nuclear ribonucleoprotein polypepti	5.4
	128793	W93562	Hs.105749	KIAA0553 protein	4.6
	128835	W15528	Hs.106390	Homo sapiens mRNA; cDNA DKFZp586	4
10	128845	AA455658	Hs.10649	basement membrane-induced gene	6.9
	128871	AA400271	Hs.106778	Homo sapiens mRNA for putative Ca2+-t	4.5
	128922	AA252023	Hs.9589	ESTs; Weakly similar to HRIHFB2157 [H	6.4
	128925	D61676	Hs.21851	Homo sapiens mRNA; cDNA DKFZp586	6.4
	128938	AA410325	Hs.107260	ESTs	7
15	128946	N29353	Hs.107318	kynurenine 3-monooxygenase (kynurenin	5.2
	128948	AA485655	Hs.223025	proteasome (prosome; macropain) subunit	13.1
	128955	F10290	Hs.185807	Homo sapiens clone 24758 mRNA sequen	5.8
	129005	AA460049	Hs.13323	ESTs; Weakly similar to SODIUM- AND	12.6
	129009	AA131421	Hs.75607	ESTs	9.8
20	129017	H13108	Hs.107968	ESTs	13.9
	129057	X62466	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	10.7
	129075	AA129465	Hs.83765	ESTs	4.7
	129095	L12350	Hs.108623	thrombospondin 2	4.4
25	129124	AA234530	Hs.108802	N-ethylmaleimide-sensitive factor	20.7
	129160	AA131252	Hs.109007	ESTs	5.9
	129164	AA282183	Hs.109045	ESTs	5.8
	129180	R40556	Hs.318401	ESTs; Highly similar to HSPC039 protein	7.6
	129224	X89109	Hs.109606	coronin; actin-binding protein; 1A	12
	129229	AA211941	Hs.109643	polyadenylate binding protein-interacting	7.9
30	129240	W24360	Hs.237868	Interleukin 7 receptor	5.3
	129241	AA435665	Hs.109706	ESTs; Moderately similar to HN1 [M.mus	8.4
	129243	H88033	Hs.109727	KIAA0733 protein	7.8
	129247	AA151574	Hs.109733	pinin-like transcription factor	6.4
	129259	AA090695	Hs.181385	ESTs	6.2
35	129270	Z35227	Hs.109918	ras homolog gene family; member H	5.4
	129281	AA026318	Hs.289101	glucose regulated protein; 58kD	4.4
	129300	C20976	Hs.110165	ESTs; Highly similar to ribosomal protein	5.7
	129318	N93155	Hs.285976	catmodulin 1 (phosphorylase kinase; delta	7.7
	129319	AA037467	Hs.30340	ESTs	6
40	129351	AA167268	Hs.62349	Human ras inhibitor mRNA; 3' end	9.3
	129366	H18027	Hs.184697	plexin C1	18.2
	129383	W92984	Hs.288224	ESTs	5.9
	129388	AA151621	Hs.110964	ESTs	4.1
	129391	T80814	Hs.11101	discs; large (Drosophila) homolog 3 (neur	10.9
45	129404	AA172056	Hs.317584	ESTs	5.3
	129406	N23707	Hs.111138	KIAA0712 gene product	4
	129426	AA412087	Hs.111323	EST; Highly similar to protein inhibitor o	8
	129453	AA421213	Hs.111632	Lsm3 protein	5.5
	129513	C00225	Hs.306163	ESTs; Weakly similar to fos39554_1 [H.s	5.5
50	129519	AA298786	Hs.112242	ESTs	6.8
	129606	R21443	Hs.166254	heat shock 90kD protein 1; alpha	5
	129622	AA278243	Hs.323949	ESTs	6.8
	129626	AA447410	Hs.111334	ESTs; Weakly similar to IIII ALU SUBFA	5.1
	129627	AA258308	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564	5.3
55	129628	U26727	Hs.1174	cyclin-dependent kinase inhibitor 2A (mel	8.2
	129642	R50008	Hs.11806	7-dehydrocholesterol reductase	4.3
	129663	AA442768	Hs.11866	translocase of inner mitochondrial membr	4.4
	129665	M88458	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic re	4
	129691	X06700	Hs.119571	collagen; type III; alpha 1 (Ehlers-Danlos	6
60	129783	AA454618	Hs.12479	associated molecule with the SH3 domain	6.4
	129800	AA252436	Hs.12540	lysophospholipase I	7.7
	129836	AA452161	Hs.206521	YME1 (S.cerevisiae)-like 1	5
	129850	N20593	Hs.288932	GDP dissociation inhibitor 2	6.9
	129869	AA102520	Hs.13015	ESTs; Weakly similar to heat shock prote	5
65	129896	AA043021	Hs.13225	UDP-GalbetaGlcNAc beta 1;4- galactosy	6.6
	129982	M87789		immunoglobulin gamma 3 (Gm marker)	4
	129985	AA450045	Hs.140452	cargo selection protein (mannose 6 phosp	5.8

	130029	AA236412	Hs.236510	ESTs; Moderately similar to PFT27 (M.m	5.6
	130033	M90696	Hs.181301	cathepsin S	5.4
	130036	AA195260	Hs.125849	ESTs; Moderately similar to IIII ALU SU	7.4
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	7.6
5	130077	T24055	Hs.91379	ribosomal protein L26	4
	130080	X14850	Hs.147097	H2A histone family; member X	12.1
	130096	AA223874	Hs.197955	KIAA0704 protein	5
	130114	AA234717	Hs.14892	ESTs	7.8
	130125	M36803	Hs.1504	hemopexin	7.2
10	130135	M61764	Hs.21635	tubulin; gamma 1	5.6
	130170	AA610070	Hs.151469	calcium/calmodulin-dependent serine pro	7.5
	130189	D43947	Hs.151761	KIAA0100 gene product	6.4
	130208	AA620556	Hs.15250	peroxisomal D3/D2-enoyl-CoA isomerase	6.4
	130211	D50840	Hs.23703	UDP-glucose ceramide glucosyltransferase	4.5
15	130235	X14046	Hs.153053	CD37 antigen	9.1
	130276	S75295	Hs.169149	karyopherin alpha 1 (importin alpha 5)	8.6
	130280	L13738	Hs.153937	activated p21cdc42Hs kinase	5
	130313	AA620323	Hs.154320	ubiquitin-activating enzyme E1C (homolo	6.1
	130314	D86967	Hs.154332	KIAA0212 gene product	10
20	130328	AA135673	Hs.154666	KIAA0391 gene product	6.1
	130356	X84373	Hs.155017	nuclear receptor interacting protein 1	10.6
	130367	Z38601	Hs.8768	ESTs; Weakly similar to III ALU SUBFA	8.3
	130378	T47333	Hs.155188	TATA box binding protein (TBP)-associa	7.1
	130384	X66364	Hs.166071	cyclin-dependent kinase 5	5.6
25	130393	D13630	Hs.155291	KIAA0305 gene product	4.1
	130399	AA449417	Hs.155356	Homo sapiens mRNA for putative glucosy	4.6
	130407	N29888	Hs.155410	ESTs	7
	130414	M21121	Hs.241392	small inducible cytokine A5 (RANTES)	4.1
	130417	U58522	Hs.155485	huntingtin-interacting protein 2	7.9
30	130421	D21260	Hs.178710	clathrin; heavy polypeptide-like 2	4
	130441	U35835	Hs.155637	protein kinase; DNA-activated; catalytic p	6.8
	130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acety)	26.4
	130498	L38951	Hs.180446	karyopherin (importin) beta 1	4.8
	130499	AA416723	Hs.158286	Homo sapiens mRNA for KIAA0446 prot	6.1
35	130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pseud	8.3
	130553	AA430032	Hs.252587	pituitary tumor-transforming 1	7.5
	130558	H96654	Hs.15984	ESTs; Weakly similar to gene pp21 protei	5.6
	130568	AA232535	Hs.16085	ESTs; Highly similar to CGI-13 protein [H	4
	130583	W24957	Hs.293907	ESTs; Moderately similar to similar to C.e	13.3
40	130585	H66211	Hs.16331	ESTs	10.1
	130604	X03635	Hs.1657	estrogen receptor 1	39.9
	130614	AA132007	Hs.16697	ESTs	5.1
	130619	AA477739	Hs.12532	ESTs	5.9
	130622	AA235247	Hs.16846	ESTs; Weakly similar to cytochrome P45	4.1
45	130625	F03969	Hs.260720	matrix metalloproteinase 2 (gelatinase A;	8.3
	130627	L23808	Hs.1695	matrix metalloproteinase 12 (macrophage	10.3
	130629	M60346	Hs.1697	ATPase; H+ transporting; lysosomal (vacu	7
	130635	M87503	Hs.1706	interferon-stimulated transcription factor	5.5
	130639	D59711	Hs.17132	ESTs	7.2
50	130677	H17861	Hs.17767	ESTs	13.5
	130681	D82808	Hs.17820	Rho-associated; coiled-coil containing pro	6
	130693	AA487202	Hs.17962	ESTs	6.1
	130703	N63295	Hs.18103	ESTs	4.3
	130706	AA488843	Hs.201673	cornichon-like	4
55	130712	AA292066	Hs.279762	adenylate cyclase 7	5.1
	130714	X92896	Hs.18212	DNA segment on chromosome X (unique)	8.4
	130715	T98227	Hs.171952	occludin	5.7
	130744	AA203527	Hs.18747	POP7 (processing of precursor; S. cerevis	6.2
	130747	AA471293	Hs.6879	ESTs	8.2
60	130751	AA435633	Hs.18879	Homo sapiens clone 23965 mRNA sequen	8.3
	130796	R39390	Hs.19525	ESTs	4.5
	130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p80 subu	7.7
	130855	AA425439	Hs.143323	putative DNA/chromatin binding motif	4.3
	130859	AA287327	Hs.20478	ceroid-lipofuscinosis; neuronal 2; late infa	9.8
65	130866	M58028	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T a	4.3
	130880	D14678	Hs.20830	kinesin-like 2	4.5
	130891	D31891	Hs.20991	SET domain; bifurcated; 1	4

	130905	AA056489	Hs.129998	ESTs	8.7
	130913	W03692	Hs.21198	translocase of outer mitochondrial membr	20.9
	130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture a	9
	130921	AA074596	Hs.194688	bromodomain adjacent to zinc finger dom	5.3
5	130944	M97935	Hs.21486	signal transducer and activator of transcrip	18.8
	130974	X57985	Hs.2178	H2B histone family; member Q	13.4
	130987	R45698	Hs.21893	ESTs; Weakly similar to cAMP inducible	8.5
	130999	N48963	Hs.21992	KIAA0689 protein	7.2
	131010	AA435748	Hs.169341	ESTs; Weakly similar to phosphatidic acid	5.2
10	131046	X02530	Hs.2248	small inducible cytokine subfamily B (Cy	10.1
	131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl peptid	6.3
	131153	H11760	Hs.23606	ESTs	7.3
	131185	M25753	Hs.23960	cyclin B1	6.2
	131200	AA609427	Hs.293732	ESTs; Moderately similar to !!! ALU SU	4.3
15	131206	AA044078	Hs.24210	ESTs	5.5
	131210	AA430047	Hs.95549	ESTs	7.1
	131227	AA429472	Hs.236522	DKFZP434P106 protein	5.6
	131244	D38076	Hs.24763	RAN binding protein 1	5.5
	131245	AA620599	Hs.24766	DKFZP564E1962 protein	6.7
20	131257	AA256042	Hs.24908	ESTs	5.8
	131319	U25997	Hs.25590	stannocalcin	8.9
	131339	AA483450	Hs.25812	Nijmegen breakage syndrome 1 (nlbrin)	6.5
	131388	R34531	Hs.92200	KIAA0480 gene product	9.2
	131410	H84658	Hs.279836	ESTs	12.1
25	131472	AA608962	Hs.27258	calcyclin binding protein	18.1
	131475	Z39053	Hs.27263	ESTs	7.5
	131501	AA121127	Hs.8207	H3 histone; family 3A	5.5
	131514	X02152	Hs.2795	lactate dehydrogenase A	5.1
	131524	N39152	Hs.301804	ESTs	4.3
30	131525	D60856	Hs.28309	UDP-glucose dehydrogenase	8.4
	131544	N33236	Hs.28555	ESTs; Weakly similar to B0511.8 [C.eleg	5.6
	131557	D30946	Hs.28707	signal sequence receptor; gamma (transloc	8.7
	131562	U90551	Hs.28777	H2A histone family; member L	18.8
	131564	AA491465	Hs.28792	ESTs	11.8
35	131586	AA235385	Hs.26966	ESTs; Moderately similar to alternatively	4.7
	131587	M15182	Hs.183858	glucuronidase; beta	5.2
	131589	U52100	Hs.29191	epithelial membrane protein 2	4.4
	131615	D14533	Hs.192803	xeroderma pigmentosum; complementatio	4.6
	131664	AA136126	Hs.30327	mitogen-activated protein kinase-activated	4.3
40	131679	AA136660	Hs.30579	ESTs	9.4
	131684	U26174	Hs.3086	granzyme K (serine protease; granzyme 3	9.7
	131687	L11066	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	6.2
	131689	AA599853	Hs.30696	transcription factor-like 5 (basic helix-loop	8.3
	131693	W60913	Hs.110796	ESTs; Weakly similar to cDNA EST yk45	9
45	131710	AA233225	Hs.30985	MRS1 protein	5.2
	131716	D49738	Hs.31053	cytoskeleton-associated protein 1	6.6
	131742	D31352	Hs.31433	ESTs	11
	131762	H46831	Hs.107767	ESTs; Moderately similar to CaM-KII inh	4.9
	131781	AA460450	Hs.31989	DKFZP586G1722 protein	9.2
50	131795	N32724	Hs.32317	Sox-like transcriptional factor	4.5
	131809	L76517	Hs.3260	presenilin 1 (Alzheimer disease 3)	5.4
	131814	AA437226	Hs.157	interleukin 10 receptor; alpha	4
	131838	AA091932	Hs.180628	dynamitin-like protein	6.7
	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	5
55	131885	AA044095	Hs.3402	ESTs	11.1
	131891	AA158258	Hs.30376	heterogeneous nuclear protein similar to r	5.6
	131925	AA248470	Hs.183180	ESTs; Weakly similar to RING finger pro	4.5
	131930	AA205460	Hs.69476	ESTs	14.3
	131941	D62657	Hs.35086	ubiquitin-specific protease 1	6.2
60	131965	W90146	Hs.35962	ESTs	6.3
	131970	D86960	Hs.3610	KIAA0205 gene product	4.2
	131971	R70167	Hs.154938	ESTs	4.3
	131974	AA410424	Hs.268122	Homo sapiens mRNA; cDNA DKFZp586	4.6
	131977	F09788	Hs.3622	procollagen-proline; 2-oxoglutarate 4-diox	6.4
65	131994	AA479515	Hs.279882	Human DNA sequence from clone 703H1	12
	131997	D82399	Hs.136844	Homo sapiens clone 23714 mRNA sequen	10
	132017	W67251	Hs.267659	Homo sapiens vav 3 oncogene (VAV3) m	4.7

	132021	T68246	Hs.306079	chaperonin containing TCP1; subunit 5 (c	5.2
	132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S sub	8.5
	132085	D44466	Hs.3887	proteasome (prosome; macropain) 26S sub	13.5
	132089	AA131971	Hs.39122	ESTs	4.8
5	132109	AA599801	Hs.40098	ESTs	6.2
	132143	AA257056	Hs.7972	KIAA0871 protein	14.6
	132149	T10822	Hs.324743	ESTs	5.3
	132153	N90141	Hs.41066	ESTs; Moderately similar to ELONGATI	9.2
10	132160	AA281770	Hs.295923	seven in absentia (Drosophila) homolog 1	5.5
	132164	U84573	Hs.41270	procollagen-lysine; 2-oxoglutarate 5-dioxy	8.1
	132180	AA405569	Hs.418	fibroblast activation protein; alpha; seprax	15.4
	132183	L19183	Hs.199695	hypothetical protein	12.2
	132225	AA128980		ESTs	5.6
	132227	AA412620	Hs.4248	ESTs	6.7
15	132235	F09058	Hs.42656	ESTs	6.2
	132256	AA608856	Hs.431	murine leukemia viral (bmi-1) oncogene h	6
	132298	N41849	Hs.7120	Homo sapiens cytokine receptor related p	5.6
	132314	AA285290	Hs.44499	small EDRK-rich factor 2	6.8
	132325	N37065	Hs.44856	ESTs	4.7
20	132384	AA479933	Hs.48967	Human DNA sequence from clone 167A1	4.2
	132387	R70914	Hs.281434	heat shock 70kD protein 1	9.1
	132393	W85688	Hs.47334	ESTs; Moderately similar to IIII ALU SU	4
	132406	F09979	Hs.4774	ESTs	15
	132407	AA431459	Hs.47783	ESTs	8
25	132413	AA132969	Hs.260116	KIAA1104 protein	4
	132446	AA426218	Hs.48764	ESTs	5.3
	132465	AA047896	Hs.49169	ESTs	15.4
	132482	AA429478	Hs.238126	ESTs; Highly similar to CGI-49 protein [H	9
	132492	T03749	Hs.4990	KIAA1089 protein	8.5
30	132528	AA283006	Hs.50758	chromosome-associated polypeptide C	4.3
	132540	AA488987	Hs.5097	synaptogyrin 2	9.8
	132543	AA417152	Hs.5101	protein regulator of cytokinesis 1	10.1
	132580	L37042	Hs.283738	casein kinase 1; alpha 1	5.9
	132586	AA412452	Hs.52515	DKFZP434N024 protein	4.2
35	132608	AA199588	Hs.5321	ARP3 (actin-related protein 3; yeast) hom	4.2
	132616	AA386264	Hs.283558	isocitrate dehydrogenase 2 (NADP+); mil	5.2
	132617	AA171913	Hs.5338	carbonic anhydrase XII	10.1
	132618	AA253330	Hs.279916	adaptor-related protein complex 1; gamma	4.8
	132640	U33821	Hs.5437	Tax1 (human T-cell leukemia virus type I	5.7
40	132668	AA453614	Hs.5460	KIAA0776 protein	4.4
	132694	M60830	Hs.5509	ecotropic viral integration site 2B	15.6
	132700	N47109	Hs.5521	ESTs	7
	132724	AA417962	Hs.55498	geranylgeranyl diphosphate synthase 1	5.6
45	132738	W42674	Hs.264636	ESTs; Moderately similar to neuronal tne	4.9
	132742	AA490862	Hs.292812	ESTs; Weakly similar to C43H8.1 [C.eleg	7.9
	132744	X54326	Hs.55921	glutamyl-prolyl-tRNA synthetase	4.1
	132795	H99152	Hs.57079	ESTs	8
	132807	AA331777	Hs.57301	mutL (E. coli) homolog 1 (colon cancer; n	8
	132811	U25435	Hs.57419	transcriptional repressor	4
50	132817	AB004884	Hs.57553	tousled-like kinase 2	6.5
	132840	N23817	Hs.5807	Homo sapiens clone 23675 mRNA sequen	5.6
	132845	D52588	Hs.5813	ESTs	12.4
	132847	T48195	Hs.58189	eukaryotic translation initiation factor 3; s	7
	132856	W79865	Hs.58367	glypican 4	6.2
55	132869	N26855	Hs.203961	ESTs	6.5
	132874	AA425776	Hs.58609	ESTs	5.6
	132880	AA444369	Hs.177537	ESTs	7.2
	132894	D82422	Hs.5944	ESTs	7.5
	132900	N56451	Hs.5978	LIM domain only 7	4.4
60	132903	AA235404	Hs.5985	Homo sapiens clone 25186 mRNA sequen	9.1
	132904	X83618	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A	10.7
	132906	AA142857	Hs.234896	ESTs; Highly similar to geminin [H.saple	10.2
	132914	AA496037	Hs.60293	ESTs	4.7
	132918	AA252605	Hs.6051	KIAA0616 protein	7.1
65	132936	AB002305	Hs.6111	KIAA0307 gene product	8.3
	132951	U04209	Hs.61418	microfibrillar-associated protein 1	4.3
	132957	AA234791	Hs.61469	Human gene from PAC 753P9; chromoso	13.2

	132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cere	18.9
	132968	N77151	Hs.61638	myosin X	5.8
	132984	H80409	Hs.62112	zinc finger protein 207	4.3
5	132990	AA458761	Hs.18387	transcription factor AP-2 alpha (activating	4.2
	132994	AA505133	Hs.279905	solute carrier family 2 (facilitated glucose	26.4
	132998	Y00062	Hs.170121	protein tyrosine phosphatase; receptor typ	4.4
	133002	AF006082	Hs.42915	ARP2 (actin-related protein 2; yeast) hom	4.7
	133005	C21400	Hs.278605	KIAA0970 protein	6.6
	133015	AA047036	Hs.246315	ESTs	7.9
10	133016	W81298	Hs.6289	growth factor receptor-bound protein 2	5.2
	133039	X62055	Hs.63489	protein tyrosine phosphatase; non-recepto	4
	133050	S67325	Hs.63788	propionyl Coenzyme A carboxylase; beta	5.2
	133056	AA071387	Hs.6396	jumping translocation breakpoint	5
	133062	R33663	Hs.64056	ESTs	5.4
15	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	6
	133091	AA122147	Hs.64691	KIAA0483 protein	5
	133093	AA598749	Hs.285996	ESTs	5.6
	133124	AA156049	Hs.267923	ESTs	4.1
	133126	D16469	Hs.6551	ATPase; H+ transporting; lysosomal (vacu	6.2
20	133196	R37367	Hs.6727	Ras-GTPase activating protein SH3 doma	5.1
	133214	Y10659	Hs.285115	interleukin 13 receptor; alpha 1	6.2
	133225	Z41415	Hs.6823	ESTs; Weakly similar to intrinsic factor-B	8.3
	133228	N90029	Hs.6831	Homo sapiens clone 1400 unknown prote	4.7
	133239	AA059405	Hs.179882	Homo sapiens clone 24655 mRNA sequen	5.5
25	133240	D31161	Hs.242894	ESTs	9
	133257	AF006066	Hs.6895	actin related protein 2/3 complex; subunit	7.7
	133264	W72187	Hs.69192	ESTs; Weakly similar to cDNA EST yk37	6.7
	133274	AA488886	Hs.6949	ESTs	4.2
	133281	AA421079	Hs.69594	ESTs; Weakly similar to Sox-like transcri	4.9
30	133283	AA410507	Hs.6968	ESTs	4.3
	133287	L15702	Hs.69771	B-factor; properdin	9.3
	133294	R79723	Hs.69997	zinc finger protein 238	30.4
	133297	AA600057	Hs.70266	KIAA0905 protein	10.4
	133318	AA256168	Hs.152316	ESTs	8.5
35	133352	H06195	Hs.7194	ESTs; Highly similar to CGI-59 protein [H	14
	133370	AA156897	Hs.72157	DKFZP564I1922 protein	5
	133391	X57579	Hs.727	inhibin; beta A (activin A; activin AB alp	13.9
	133395	AA491296	Hs.72805	ESTs	4.3
	133422	N79516	Hs.73287	ESTs; Weakly similar to eyelid [D.melano	4.5
40	133431	AA255436	Hs.7358	Homo sapiens mRNA; cDNA DKFZp586	8
	133435	T23983	Hs.323966	ESTs	5
	133449	AA094989	Hs.7381	voltage-dependent anion channel 3	8.7
	133468	X03068	Hs.73931	major histocompatibility complex; class II	5
	133484	X78710	Hs.211581	metal-regulatory transcription factor 1	5.3
45	133505	AA316868	Hs.74346	ESTs; Weakly similar to 140G11.h [D.me	6.8
	133517	X52947	Hs.74471	gap junction protein; alpha 1; 43kD (conn	5.7
	133551	D63480	Hs.278634	KIAA0146 protein	4.8
	133569	AA313977	Hs.172772	transcription elongation factor B (SIII); po	9.5
	133572	W94333	Hs.279915	translocase of inner mitochondrial membr	5
50	133577	F03717	Hs.75063	human immunodeficiency virus type I enh	7.4
	133589	L37368	Hs.75104	RNA-binding protein S1; serine-rich dom	5
	133608	D13315	Hs.75207	glyoxalase I	4.2
	133617	AA148318	Hs.75249	KIAA0069 protein	4.5
	133627	U09587	Hs.75280	glycyl-tRNA synthetase	10
55	133633	D21262	Hs.75337	nucleolar phosphoprotein p130	4.5
	133634	U24166	Hs.234279	microtubule-associated protein; RP/EB fa	15.2
	133640	D83004	Hs.75355	ubiquitin-conjugating enzyme E2N (homo	9.1
	133644	D89077	Hs.75367	Src-like-adaptor	6.4
	133649	AA479139	Hs.75393	acid phosphatase 1; soluble	4.8
60	133652	AA287383	Hs.7540	ESTs	4.2
	133674	AA458946	Hs.75497	ESTs	4.3
	133700	K01396	Hs.297681	protease inhibitor 1 (anti-elastase); alpha-	8.3
	133705	N21648	Hs.75659	MpV17 transgene; murine homolog; glom	4.6
	133716	Y00282	Hs.75722	ribophorin II	7.5
65	133720	L27841	Hs.75737	pericentriolar material 1	9.4
	133752	U49278	Hs.75875	ubiquitin-conjugating enzyme E2 variant	4.5
	133765	D21255	Hs.75929	cadherin 11 (OB-cadherin; osteoblast)	6.4

	133772	W73693	Hs.76038	isopentenyl-diphosphate delta isomerase	7.9
	133774	Z23090	Hs.76067	heat shock 27kD protein 1	4.1
	133776	J03473	Hs.177766	ADP-ribosyltransferase (NAD+; poly (AD	13
	133784	AA214305	Hs.301064	ESTs	5.2
5	133814	M33882	Hs.76391	myxovirus (influenza) resistance 1; homol	11.7
	133829	AA453783	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564	9.4
	133834	AA147510	Hs.288660	serine protease; umbilical endothelium	4.8
	133839	M59815	Hs.170250	complement component 4A	6.7
	133842	U73477	Hs.285013	putative human HLA class II associated p	7.1
10	133845	T68510	Hs.76704	ESTs	6.3
	133859	U66782	Hs.178761	26S proteasome-associated pad1 homolog	13.7
	133867	D43948	Hs.76989	KIAA0097 gene product	4.1
	133868	U58090	Hs.183874	cullin 4A	4
	133871	AA454597	Hs.182793	ESTs	4.7
15	133893	X01060	Hs.77356	transferrin receptor (p90; CD71)	8.3
	133914	N32811	Hs.77542	ESTs	5
	133918	W72783	Hs.58382	ESTs; Weakly similar to C13F10.5 [C.ele	4.5
	133944	AA045870	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564	6.3
	133946	AA156565	Hs.173878	4-nitrophenylphosphatase domain and non	6.4
20	133963	L34587	Hs.184693	transcription elongation factor B (SIII); po	6.3
	133980	D00760	Hs.250811	proteasome (prosome; macropain) subunit	11.9
	133990	C02374	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564	8.2
	133999	M28213	Hs.78305	RAB2; member RAS oncogene family	5.2
	134030	J03077	Hs.78575	prosaposin (variant Gaucher disease and v	4.6
25	134032	Z81326	Hs.78589	protease inhibitor 12 (neuroserpin)	6.5
	134045	S82470	Hs.78768	BB1	11.9
	134046	D28473	Hs.172801	isoleucine-tRNA synthetase	5.2
	134064	D87685	Hs.78893	KIAA0244 protein	7.3
	134070	H98621	Hs.78946	cullin 3	4.7
30	134087	U51166	Hs.173824	thymine-DNA glycosylase	7
	134090	M22382	Hs.79037	heat shock 60kD protein 1 (chaperonin)	4.5
	134098	X06323	Hs.79066	ribosomal protein; mitochondrial; L3	9.4
	134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	4.4
	134132	U32519	Hs.220689	Ras-GTPase-activating protein SH3-doma	6.6
35	134168	AA398908	Hs.181634	Human Chromosome 16 BAC clone CIT9	8.6
	134170	M63138	Hs.79572	cathepsin D (lysosomal aspartyl protease)	9.3
	134208	U88871	Hs.79993	peroxisomal biogenesis factor 7	6.3
	134258	L28010	Hs.808	heterogeneous nuclear ribonucleoprotein F	4.3
	134288	AA430008	Hs.8117	ESTs	6.9
40	134310	AA313414	Hs.8148	Homo sapiens clone 24856 mRNA sequen	7.4
	134326	U16306	Hs.81800	chondroitin sulfate proteoglycan 2 (versic	6.1
	134329	D38551	Hs.81848	RAD21 (S. pombe) homolog	8.6
	134331	AA452020	Hs.111222	ESTs; Weakly similar to CGI-128 protein	6.1
	134351	R82074	Hs.82109	syndecan 1	4.4
45	134357	L43675	Hs.82171	Human clone 191B7 placenta expressed m	6.6
	134363	M37033	Hs.82212	CD53 antigen	5.3
	134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfe	4.8
	134374	D62633	Hs.8236	ESTs	15.2
	134375	AA412720	Hs.82389	ESTs; Highly similar to CGI-118 protein	7.2
50	134376	X02874	Hs.82396	2';5'-oligoadenylate synthetase 1	6.4
	134381	U56637	Hs.184270	capping protein (actin filament) muscle Z-	4
	134388	M15841	Hs.82575	small nuclear ribonucleoprotein polypepti	5.7
	134395	L09717	Hs.8262	lysosomal-associated membrane protein 2	6.9
	134399	H99801	Hs.82689	tumor rejection antigen (gp96) 1	4.5
55	134401	AA243746	Hs.211577	kinecin 1 (kinesin receptor)	11.2
	134405	J04177	Hs.82772	collagen; type XI; alpha 1	15.3
	134415	AA329274	Hs.82911	protein tyrosine phosphatase type IVA; m	4.1
	134417	D87989	Hs.82921	solute carrier family 35 (CMP-sialic acid t	4.2
	134419	L08044	Hs.82961	trefoil factor 3 (intestinal)	5.9
60	134421	AA122386	Hs.82985	collagen; type V; alpha 2	5.8
	134423	W96151	Hs.83006	ESTs; Highly similar to CGI-139 protein	4.4
	134438	AA449984	Hs.246857	ESTs; Highly similar to protein kinase JN	7
	134446	T25732	Hs.83419	KIAA0252 protein	4.6
	134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	5.1
65	134470	X54942	Hs.83758	CDC28 protein kinase 2	20.3
	134487	R38185	Hs.83954	Homo sapiens unknown mRNA	5
	134495	D63477	Hs.84087	KIAA0143 protein	16.1

	134498	M63180	Hs.84131	threonyl-tRNA synthetase	6.1
	134506	U45328	Hs.84285	ubiquitin-conjugating enzyme E21 (homol	4.6
	134529	H24460	Hs.848	FK506-binding protein 4 (59kD)	6.2
	134570	U66615	Hs.172280	SWI/SNF related; matrix associated; actin	4.8
5	134582	AA234966	Hs.86041	CGG triplet repeat binding protein 1	4.7
	134600	R68884	Hs.86347	ESTs; Weakly similar to predicted using G	5.8
	134623	X74496	Hs.86978	prolyl endopeptidase	4.5
	134654	W23625	Hs.8739	ESTs; Weakly similar to ORF YGR200c [13.7
	134655	AA454070	Hs.123090	ESTs	5.8
10	134675	AA250745	Hs.87773	protein kinase; cAMP-dependent; catalyti	8.9
	134711	X04011	Hs.88974	cytochrome b-245; beta polypeptide (chro	6.8
	134714	U89922	Hs.890	lymphotoxin beta (TNF superfamily; mem	35.7
	134722	W47183	Hs.284226	ESTs; Weakly similar to neural F box pro	8.1
	134776	J05582	Hs.89603	mucin 1; transmembrane	6.2
15	134806	Z49099	Hs.89718	spermine synthase	4.2
	134810	M27394	Hs.89751	membrane-spanning 4-domains; subfamily	7
	134840	U51477	Hs.89981	diacylglycerol kinase; zeta (104kD)	4.1
	134843	H60595	Hs.90061	progesterone binding protein	4.7
	134853	D82348	Hs.90280	5-aminimidazole-4-carboxamide ribonuc	10.2
20	134866	U84011	Hs.904	amylase-1;6-glucosidase; 4-alpha-glucanot	12.1
	134868	Z39762	Hs.90419	KIAA0882 protein	6
	134885	N27670	Hs.9071	progesterone membrane binding protein	5
	134982	N46086	Hs.92308	ESTs	4.1
	134989	AA236324	Hs.92381	Homo sapiens mRNA; chromosome 1 spe	16.8
25	134992	H05625	Hs.5831	ESTs	4
	134993	AA282343	Hs.301005	purine-rich element binding protein B	4.4
	135010	D59675	Hs.92927	ESTs	7
	135015	U54999	Hs.278338	LGN protein	4.8
	135029	AA224180		ESTs; Moderately similar to 17-beta-hydr	13.6
30	135032	AA243497	Hs.173685	Human DNA sequence from clone 30M3	4
	135037	U77948	Hs.278589	general transcription factor II; i	8
	135059	AA598449	Hs.93832	Homo sapiens clone 24483 unknown mRN	5.4
	135071	L08069	Hs.94	heat shock protein; DNAJ-like 2	9.3
	135083	AA495950	Hs.94262	ESTs	6.7
35	135117	W52493	Hs.94694	Homo sapiens clone 24837 mRNA sequen	10.2
	135144	AA044842	Hs.95260	Homo sapiens mRNA; cDNA DKFZp586	6.6
	135154	AA126433	Hs.267812	sorting nexin 4	7.4
	135218	D31157	Hs.324277	ESTs; Weakly similar to growth factor-res	6.2
	135237	AA454930	Hs.9691	ESTs	19.5
40	135243	AA215333	Hs.97101	putative G protein-coupled receptor	8.8
	135335	H20989	Hs.198281	pyruvate kinase; muscle	12.4
	135349	D83174	Hs.9930	collagen-binding protein 2 (collagen 2)	5.5
	135367	AA480109	Hs.9963	TYRO protein tyrosine kinase binding pro	5.4
	135389	U05237	Hs.99872	fetal Alzheimer antigen	7.8
45	135400	M23263	Hs.99915	androgen receptor (dihydrotestosterone re	9.1
	135411	L10333	Hs.99947	reticulum 1	5.3
	300019	M97935		AFFX control: STAT1	8.3
	300021	M97935		AFFX control: STAT1	7
	300022	M97935		AFFX control: STAT1	14
50	300069	AI199738	Hs.208275	ESTs; Weakly similar to IIII ALU CLASS	9.1
	300107	AI694585	Hs.270484	ESTs; Weakly similar to IIII ALU CLASS	7.4
	300254	AW079607	Hs.188417	ESTs; Weakly similar to ZnT-3 [H.sapien	30.1
	300328	AW015860	Hs.224623	ESTs	11.9
	300549	AA699328	Hs.298119	ESTs	5.5
55	300711	AI492179	Hs.166244	ESTs; Weakly similar to cDNA EST yk40	11
	300921	AW293224	Hs.232165	ESTs	11
	301124	T79326	Hs.298262	ESTs; Weakly similar to dJ88J8.1 [H.sapi	8.8
	301165	N85789	Hs.150186	ESTs; Weakly similar to PTERIN-4-ALP	6
	301576	AI682905	Hs.270431	ESTs; Weakly similar to IIII ALU SUBFA	4.7
60	301604	AA373124	Hs.24809	ESTs; Weakly similar to C17G10.1 [C.ete	8
	301704	AA526313	Hs.293691	ESTs	4.2
	301782	N99399	Hs.143046	EST cluster (not in UniGene) with exon h	18
	301884	AA312082	Hs.105445	GDNF family receptor alpha 1	20.7
	301936	NM_004694	Hs.114924	EST cluster (not in UniGene) with exon h	11.6
65	302002	AF013956	Hs.5637	chromobox homolog 4 (Drosophila Pc cla	9.2
	302032	NM_001892	Hs.128087	EST cluster (not in UniGene) with exon h	4.3
	302057	H05698	Hs.222399	ESTs; Weakly similar to protein-tyrosine	7.8

5	302145	NM_003613	Hs.151407	EST cluster (not in UniGene) with exon h	15.1
	302236	AI128606	Hs.6557	zinc finger protein 161	25.8
	302276	NM_004448	Hs.323910	EST cluster (not in UniGene) with exon h	21.6
	302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564	41.4
	302326	NM_004271	Hs.184018	EST cluster (not in UniGene) with exon h	8.9
10	302342	AB023141	Hs.190386	KIAA0924 protein	5.4
	302372	AL117406	Hs.200102	Homo sapiens mRNA; cDNA DKFZp434	8.9
	302422	AB021227	Hs.3743	matrix metalloproteinase 24 (membrane-in	5.2
	302431	AF129530	Hs.226434	EST cluster (not in UniGene) with exon h	5.3
	302501	AF022726	Hs.251446	EST cluster (not in UniGene) with exon h	9.9
15	302505	AL049650	Hs.247874	multiple UniGene matches	4.3
	302533	L36149	Hs.248116	chemokine (C motif) XC receptor 1	4.9
	302638	AA463798	Hs.102696	ESTs; Weakly similar to C11D2.4 [C.eleg	5.3
	302656	AW293005	Hs.70704	ESTs	8.4
	302792	AA343696	Hs.46821	ESTs; Weakly similar to putative [H.sapie	4.5
20	302820	X04588	Hs.85844	EST cluster (not in UniGene) with exon h	6.8
	302838	U66049	Hs.82171	EST cluster (not in UniGene) with exon h	8.4
	302892	N58545	Hs.42346	histone deacetylase 3	22.8
	302977	AW263124	Hs.315111	EST cluster (not in UniGene) with exon h	6.8
	302989	N46406	Hs.84700	EST cluster (not in UniGene) with exon h	8.9
25	303007	AA478876	Hs.317714	pallid (mouse) homolog; pallidin	10.1
	303052	AF140242	Hs.279926	EST cluster (not in UniGene) with exon h	24.4
	303131	AW081061	Hs.103180	actin-like 6	6.3
	303132	AI029819	Hs.4055	ESTs	17.7
	303153	U09759	Hs.246857	mitogen-activated protein kinase 9	11.4
30	303387	AA908797	Hs.180799	ESTs	15.8
	303499	AI815990	Hs.293515	ESTs	7.2
	303502	AA488528		EST cluster (not in UniGene) with exon h	5.3
	303576	T07216	Hs.301226	EST cluster (not in UniGene) with exon h	16.2
	303620	AA397546	Hs.119151	ESTs	8.9
35	303634	AI953377	Hs.28444	ESTs; Weakly similar to predicted using G	12
	303642	AW299459	Hs.111977	EST cluster (not in UniGene) with exon h	4.2
	303654	AA436942	Hs.288529	ESTs	8.4
	303733	AW502498	Hs.15220	ESTs; Weakly similar to zinc finger prote	5.2
	303780	AI424014	Hs.18995	ESTs; Moderately similar to KIAA0456 p	28.4
40	303792	C75094	Hs.199839	ESTs; Highly similar to NG22 [H.sapiens	4.4
	303842	AI337304	Hs.126266	ESTs; Weakly similar to similar to PDZ d	8.1
	303951	AW475081	Hs.172928	collagen; type I; alpha 1	7.5
	304465	AA421948		EST singleton (not in UniGene) with exon	6.5
	304507	AA456426		EST	5.4
45	304591	AA505702		EST singleton (not in UniGene) with exon	9.8
	304601	AA507875		EST singleton (not in UniGene) with exon	7.5
	304659	AA533185		EST singleton (not in UniGene) with exon	7
	305040	AA630582	Hs.169476	glyceraldehyde-3-phosphate dehydrogena	12.4
	305134	AA653159	Hs.179661	EST singleton (not in UniGene) with exon	8.7
50	305415	AA725116	Hs.78465	EST singleton (not in UniGene) with exon	5.3
	305453	AA738110		EST singleton (not in UniGene) with exon	4.1
	305898	AA872838		keratin 8	7.7
	305913	AA876109		EST singleton (not in UniGene) with exon	6.3
	305950	AA884479		EST singleton (not in UniGene) with exon	5.6
55	306004	AA889992	Hs.2186	EST singleton (not in UniGene) with exon	13.2
	306009	AA894560	Hs.283370	EST singleton (not in UniGene) with exon	4.4
	306060	AA906161	Hs.76277	EST singleton (not in UniGene) with exon	4.6
	306398	AA970548	Hs.297681	EST singleton (not in UniGene) with exon	7.6
	306505	AA987722	Hs.172928	EST singleton (not in UniGene) with exon	19.7
60	306576	AA995761	Hs.276092	EST singleton (not in UniGene) with exon	5.5
	307117	AI184111	Hs.76067	heat shock 27kD protein 1	7.7
	307138	AI185516	Hs.172928	collagen; type I; alpha 1	8.8
	307187	AI190870	Hs.276417	EST singleton (not in UniGene) with exon	4.1
	307542	AI280859	Hs.62954	EST singleton (not in UniGene) with exon	6
65	307554	AI281603	Hs.172928	EST singleton (not in UniGene) with exon	10.8
	307806	AI351739	Hs.276726	EST singleton (not in UniGene) with exon	4.7
	308079	AI472733	Hs.270208	ESTs	4.2
	308307	AI581398	Hs.172928	collagen; type I; alpha 1	5.4
	308511	AI687580	Hs.169476	EST singleton (not in UniGene) with exon	10.1
	308615	AI738593	Hs.101774	EST singleton (not in UniGene) with exon	15.1
	308677	AI761173		EST singleton (not in UniGene) with exon	4.6

	308852	AI829848	Hs.182937	peptidylprolyl isomerase A (cyclophilin A)	5.9
	308974	AI872290	Hs.300697	immunoglobulin gamma 3 (Gm marker)	4.5
	308981	AI873242		EST singleton (not in UniGene) with exon	7.6
	308995	AI880172		EST singleton (not in UniGene) with exon	6.6
5	309177	AI951118		EST singleton (not in UniGene) with exon	24.3
	309186	AI952723	Hs.90207	EST singleton (not in UniGene) with exon	6.1
	309198	AI955915		major histocompatibility complex; class I;	5.6
	309226	AI969897		EST singleton (not in UniGene) with exon	6.2
	309279	AI990102		EST singleton (not in UniGene) with exon	7.9
10	309583	AW170035		EST	64.5
	309624	AW191929	Hs.252989	EST	5.3
	309629	AW192764	Hs.172928	collagen; type I; alpha 1	6.9
	309641	AW194230	Hs.253100	EST	11.4
	309698	AW238461	Hs.73742	ribosomal protein; large; P0	4.3
15	309700	AW241170	Hs.179661	Homo sapiens clone 24703 beta-tubulin m	11.9
	310073	AI335004	Hs.148558	ESTs	4.2
	310094	AW450967	Hs.235240	ESTs	5.7
	310373	AW080778	Hs.145582	ESTs	4.8
	310438	AW022192	Hs.200197	ESTs	39.1
20	310470	AI281848	Hs.194691	ESTs	4.9
	310583	AW205632	Hs.211198	ESTs	7
	310877	T47784	Hs.188955	ESTs	4.1
	311067	AI587332	Hs.209115	ESTs	11.2
	311166	AI821294	Hs.118599	ESTs	24.1
25	311199	T57896	Hs.191095	EST cluster (not in UniGene)	5.7
	311465	AI758660	Hs.206132	ESTs	15.7
	311587	AI828254	Hs.271019	ESTs	6.4
	311774	AA700870	Hs.14304	ESTs	6.2
	311785	AI058769	Hs.133512	ESTs	5
30	311923	T60843	Hs.189679	ESTs	5.9
	311935	AA216387		EST cluster (not in UniGene)	5.5
	311972	N51511	Hs.188449	ESTs	5.2
	312014	AI435650	Hs.128778	ESTs	4.3
	312047	AA588275	Hs.180669	ESTs	14.7
35	312147	T89855	Hs.195648	EST cluster (not in UniGene)	9.8
	312153	AA759250	Hs.153028	cytochrome b-561	27.1
	312168	T92251	Hs.198882	ESTs	4.2
	312172	AI222168	Hs.191168	ESTs	6.1
	312226	AI796815	Hs.199993	ESTs; Weakly similar to ubiquitous TPR	5.5
40	312292	AW451893	Hs.151124	ESTs	18.4
	312312	AI080505	Hs.134529	ESTs	11.9
	312369	AA582039	Hs.173884	Homo sapiens mRNA; chromosome 1 spe	4
	312407	R46180	Hs.153485	ESTs	13.6
	312430	AW139117	Hs.117494	ESTs	4.1
45	312470	AW451347	Hs.175862	ESTs	4.6
	312483	AI417526	Hs.7753	ESTs	15.3
	312521	AA033609	Hs.319093	ESTs	12.5
	312544	AI498371	Hs.183526	ESTs	14.6
	312638	AW439195	Hs.256880	ESTs	5.3
50	312754	R99834	Hs.250383	ESTs	8.4
	312772	H63791		EST cluster (not in UniGene)	4.3
	312821	AA699325	Hs.269880	ESTs	8.3
	312837	AW292286	Hs.255058	ESTs	7.1
	312849	AA846353	Hs.194054	ESTs	5.9
55	312854	AA828713	Hs.321058	EST cluster (not in UniGene)	4.1
	312992	AA088446	Hs.170298	ESTs	7.3
	313096	AI422367	Hs.163533	ESTs	6.1
	313112	AA732534	Hs.269099	ESTs	4.2
	313126	AA720887	Hs.283313	EST cluster (not in UniGene)	18.1
60	313136	N59284	Hs.288010	ESTs	17
	313197	AI738851	Hs.222487	ESTs	12.9
	313219	N74924	Hs.182099	ESTs	7.1
	313258	AW068358	Hs.183918	ESTs	13.7
	313328	AW449211	Hs.105445	ESTs	27.9
65	313352	AW292127	Hs.144758	ESTs	9.8
	313417	AA741151	Hs.137323	ESTs	8.2
	313455	AW081702	Hs.98571	ESTs	6.9

	313590	AA804410	Hs.291677	EST cluster (not in UniGene)	5.3
	313663	A1953261	Hs.169813	ESTs	7.6
	313667	U69201	Hs.13684	ESTs; Weakly similar to choline kinase is	12.5
5	313749	AW450376	Hs.119004	ESTs	5.5
	313832	AW271022	Hs.133294	ESTs	4.3
	313881	AA535580	Hs.16331	ESTs	7.7
	313915	A1969390	Hs.163443	ESTs	27.1
	313955	A1858884	Hs.270647	ESTs	5.7
	313974	A1310151	Hs.173524	ESTs	4.3
10	314097	AA648744	Hs.269493	ESTs	14.5
	314129	AA228366	Hs.115122	ESTs	9.5
	314359	AA205569	Hs.194193	ESTs	5.4
	314384	AA535840	Hs.162203	ESTs; Weakly similar to alternatively spli	5.3
	314394	A1380563	Hs.130816	ESTs	13.2
15	314462	AA347951	Hs.326413	ESTs	6.2
	314465	AA802917	Hs.156974	ESTs	18.1
	314470	A1934422	Hs.30661	ESTs	4.2
	314488	AA358265	Hs.182890	ESTs	6.1
	314506	AA833655	Hs.206868	ESTs	27.8
20	314510	A1204418	Hs.190080	ESTs	9.5
	314558	A1873274	Hs.190721	ESTs	22.5
	314661	AA436432	Hs.324239	EST cluster (not in UniGene)	13.3
	314691	AW207206	Hs.136319	ESTs	21.4
	314754	AW026761	Hs.134374	ESTs	4.4
25	314775	A1149880	Hs.188609	ESTs	4.4
	314943	A1476797	Hs.184572	cell division cycle 2; G1 to S and G2 to M	18.4
	314961	AW008061	Hs.231994	ESTs	10.2
	314963	A1689617	Hs.200934	ESTs	5.3
	315006	A1538613	Hs.298241	ESTs	20.7
30	315010	AA531082	Hs.240049	ESTs	5
	315019	AA532807	Hs.105822	ESTs	6.1
	315033	A1493046	Hs.146133	ESTs	12
	315036	AA534953	Hs.163297	ESTs	8.3
	315037	AW205863	Hs.133988	ESTs; Weakly similar to gene MAC25 pr	6.1
35	315051	AW292425	Hs.163484	EST	12.7
	315054	A1968598	Hs.78768	ESTs	7.6
	315073	AW452948	Hs.257631	ESTs	13.9
	315080	AA744550	Hs.136345	ESTs	4.4
	315083	A1221325	Hs.205442	ESTs	5.1
40	315088	AA557351	Hs.152448	ESTs; Moderately similar to MULTIFUN	4.7
	315175	A1025842	Hs.152530	ESTs	11.9
	315196	AA872756	Hs.44898	ESTs	28.8
	315296	AA876905	Hs.125286	ESTs	16.1
	315303	AW194364	Hs.128022	ESTs; Weakly similar to FIG-1 PROTEIN	25.7
45	315352	AA604799	Hs.136528	ESTs; Moderately similar to III ALU SU	12.3
	315364	AA643602	Hs.155485	ESTs; Highly similar to serine protease [H	4.6
	315368	AW291563	Hs.104696	ESTs	4.8
	315390	A1801565	Hs.200113	ESTs; Weakly similar to alternatively spli	4.4
	315408	AW273261	Hs.216292	ESTs	5
50	315458	AA872000	Hs.116104	ESTs	7.6
	315472	AA828850	Hs.165469	ESTs	4.9
	315478	AA665612	Hs.120874	ESTs	5.2
	315498	AA628539	Hs.116252	ESTs; Moderately similar to III ALU SU	4.8
	315527	A1791138	Hs.116768	ESTs	4.4
55	315530	A1200852	Hs.127780	ESTs	22.4
	315562	AA737415	Hs.152826	ESTs	5.9
	315634	AA837085	Hs.220585	ESTs	8.8
	315647	AA648983	Hs.212911	ESTs	15
	315652	A1521489	Hs.3053	ESTs	6.3
60	315676	AW002565	Hs.124660	ESTs	9.2
	315680	AA814309	Hs.123583	ESTs	8.1
	315735	A1831760	Hs.155111	ESTs	13.4
	315741	AA812188	Hs.122559	ESTs	5.4
	315769	AA744875	Hs.189413	ESTs	4.4
65	315976	AA830893	Hs.119769	ESTs	10.4
	315984	A1015862	Hs.131793	ESTs	5
	316042	AW297979	Hs.170698	ESTs	14.7

	316136	AA830808	Hs.124366	ESTs	4
	316177	AI908272	Hs.293102	EST cluster (not in UniGene)	32.6
	316313	AA741300	Hs.202599	ESTs	4.8
	316405	AA757900	Hs.270823	ESTs	4.8
5	316480	AI749921	Hs.205377	ESTs	12.9
	316564	AI743571	Hs.168799	ESTs; Weakly similar to !!!! ALU SUBFA	8.1
	316714	AA809792	Hs.123307	ESTs	5
	316715	AI440265	Hs.170673	ESTs	4.2
	316828	AA828116	Hs.173076	ESTs	5.2
10	316869	AI954880	Hs.134604	ESTs	13.3
	316905	AW138241	Hs.210846	ESTs	6.2
	316943	AW014875	Hs.137007	ESTs	5.3
	316949	AA856749	Hs.124620	ESTs	7.2
	317008	AW051597	Hs.143707	ESTs	4.1
15	317028	AA962623	Hs.189144	ESTs; Weakly similar to RENAL SODIU	4.2
	317067	AI805392	Hs.325335	ESTs	4.5
	317069	AI732892	Hs.190489	ESTs	6.4
	317210	AA490718		EST cluster (not in UniGene)	4.4
	317298	AI922374	Hs.158549	ESTs	5.9
20	317658	AW139077	Hs.202217	ESTs	4.6
	317674	AW294909	Hs.132208	ESTs	5.2
	317685	AI798630	Hs.149997	ESTs	4.3
	317836	AA983913	Hs.128929	ESTs	12.4
	317881	AI827248	Hs.224398	ESTs	12.1
25	317902	AI828602	Hs.211265	ESTs	8.8
	317916	AI565071	Hs.159983	ESTs	12.6
	318042	AW294522	Hs.149991	ESTs	5.6
	318053	AI074465	Hs.133469	ESTs	4
	318064	AW295888	Hs.170939	ESTs	5.2
30	318070	AI024594	Hs.248942	ESTs	4.7
	318073	AW167087	Hs.131562	ESTs	15.7
	318146	AI040125	Hs.150521	ESTs	5.9
	318186	AW016773	Hs.3709	ESTs	5.3
	318481	AI291584	Hs.145921	ESTs; Weakly similar to HYPOTHETICA	7.6
35	318566	AI335361	Hs.226376	ESTs	5.8
	318617	AW247252	Hs.75514	nucleoside phosphorylase	11.1
	318662	AI285898	Hs.294014	ESTs	16.3
	318691	AW192139	Hs.181307	H3 histone; family 3A	4
	318740	NM_002543	Hs.77729	EST cluster (not in UniGene)	21.3
40	318744	AI793124	Hs.144479	ESTs	35
	318948	AA317274	Hs.13996	ESTs	11.7
	319163	F15257	Hs.27	glycine dehydrogenase (decarboxylating;	7
	319478	R06841	Hs.270307	EST cluster (not in UniGene)	8.9
	319545	R83716	Hs.14355	ESTs	8.2
45	319668	NM_002731	Hs.87773	EST cluster (not in UniGene)	25.4
	319763	AA460775	Hs.6295	ESTs	7
	319913	AA179304	Hs.271586	ESTs; Moderately similar to !!!! ALU SU	8.7
	319936	W22152	Hs.282929	EST cluster (not in UniGene)	5.6
	319951	AA307665	Hs.14559	ESTs	4.9
50	319962	H06350	Hs.135056	ESTs	9.2
	319977	AA632632		EST cluster (not in UniGene)	4.6
	320074	AA321166	Hs.278233	EST cluster (not in UniGene)	16.7
	320092	AF022799	Hs.113292	calpain 9 (nCL-4)	5.4
	320107	AA836461	Hs.291712	EST cluster (not in UniGene)	5.3
55	320133	D63271		EST cluster (not in UniGene)	5.5
	320167	AA984373	Hs.90790	EST cluster (not in UniGene)	15
	320187	T99949	Hs.303428	EST cluster (not in UniGene)	6.7
	320211	AL039402	Hs.125783	DEME-6 protein	24.3
	320401	U90449	Hs.152717	nucleoside diphosphate kinase type 6 (lnh	10
60	320458	AI884396	Hs.24131	ESTs	5.4
	320488	R31386	Hs.191791	EST cluster (not in UniGene)	4.9
	320521	N31464	Hs.24743	ESTs	9.5
	320661	AA864846	Hs.115175	EST cluster (not in UniGene)	6.6
	320691	R61576	Hs.313951	hypothetical protein	5.9
65	320699	R63161	Hs.118249	EST cluster (not in UniGene)	4
	320727	U96044	Hs.181125	EST cluster (not in UniGene)	15.3
	320993	AL050145	Hs.225986	Homo sapiens mRNA; cDNA DKFZp586	7.2

	321012	AA737314	Hs.194324	EST cluster (not in UniGene)	6.1
	321050	AW393497		EST cluster (not in UniGene)	5
	321051	AF134149	Hs.240395	EST cluster (not in UniGene)	11.4
	321171	AI769410	Hs.221461	ESTs	7.7
5	321192	AA295304	Hs.297939	ESTs; Weakly similar to neogenin [H.sap	5.5
	321354	AA078493		EST cluster (not in UniGene)	16.9
	321387	H68014	Hs.141278	ESTs; Weakly similar to !!!! ALU SUBFA	4.2
	321412	AW366305	Hs.22891	EST cluster (not in UniGene)	6.3
	321489	AW392474	Hs.172759	ESTs; Moderately similar to !!!! ALU SU	9
10	321539	N98619	Hs.42915	ARP2 (actin-related protein 2; yeast) hom	11.3
	321593	H84762	Hs.253197	ESTs	10.4
	321666	D28390	Hs.272897	EST cluster (not in UniGene)	19.9
	321891	AW157424	Hs.165954	ESTs	5.6
	321910	H67065	Hs.271530	ESTs; Weakly similar to !!!! ALU SUBFA	5.4
15	321953	AW068268	Hs.292833	ESTs; Weakly similar to !!!! ALU CLASS	6.5
	321978	N77342	Hs.21851	EST cluster (not in UniGene)	10.2
	322017	AA310039	Hs.9192	ESTs	9.8
	322026	AA233527	Hs.283675	low density lipoprotein receptor (familial	27.8
	322035	AL137517	Hs.306201	EST cluster (not in UniGene)	40.2
20	322171	AF085968	Hs.48474	EST cluster (not in UniGene)	5.7
	322175	AF085975		EST cluster (not in UniGene)	7.7
	322236	AL134970	Hs.104222	folliculin-like 1	14.4
	322303	W07459	Hs.157601	EST cluster (not in UniGene)	13.4
	322735	AA086123	Hs.297856	EST cluster (not in UniGene)	7.6
25	322777	AA679082	Hs.269947	ESTs	4.4
	322818	AW043782	Hs.293616	ESTs	21
	322882	AW248508	Hs.279727	DiGeorge syndrome critical region gene 2	15.3
	322975	C16391		EST cluster (not in UniGene)	21.3
	322991	C18965	Hs.159473	ESTs	11.7
30	323011	AA580288		EST cluster (not in UniGene)	8.9
	323091	AW014094	Hs.210761	ESTs	10.8
	323107	AI301107	Hs.150790	ESTs	6.5
	323136	AL120351	Hs.30177	EST cluster (not in UniGene)	5.5
	323168	AL120862	Hs.124165	ESTs	17.9
35	323195	AI064982	Hs.117950	multifunctional polypeptide similar to SA	5.8
	323201	AL049370	Hs.13350	Homo sapiens mRNA; cDNA DKFZp586	11.6
	323203	AA203135	Hs.130186	ESTs	6.4
	323243	W44372	Hs.110771	EST cluster (not in UniGene)	7.3
	323244	T70731	Hs.193620	EST cluster (not in UniGene)	15.8
40	323328	AA228078	Hs.255096	EST cluster (not in UniGene)	4.8
	323332	AI829520	Hs.227513	ESTs	20.2
	323333	AA228883	Hs.208558	EST cluster (not in UniGene)	8.8
	323570	AL038623	Hs.208752	ESTs; Weakly similar to !!!! ALU SUBFA	5
	323604	AI751438	Hs.41271	ESTs; Weakly similar to !!!! ALU SUBFA	6.5
45	323685	AA344205	Hs.289088	EST cluster (not in UniGene)	7.1
	323753	AA327102	Hs.70266	EST cluster (not in UniGene)	6.1
	323817	AA410943		EST cluster (not in UniGene)	16.8
	323845	AI684674	Hs.41127	ESTs; Weakly similar to waclaw [D.melan	10.1
	323930	AA570698	Hs.8173	ESTs	6.4
50	323997	AA844907	Hs.274454	EST cluster (not in UniGene)	8
	324047	AA378201	Hs.271340	EST cluster (not in UniGene)	6.3
	324261	AL044891	Hs.269350	EST cluster (not in UniGene)	50.1
	324302	AA543008	Hs.292471	ESTs; Weakly similar to !!!! ALU SUBFA	5.7
	324338	AL138357	Hs.145078	ESTs	9.5
55	324344	AW502000	Hs.46677	EST cluster (not in UniGene)	4.4
	324432	AA484510	Hs.152812	EST cluster (not in UniGene)	16.7
	324495	AW501411	Hs.122489	ESTs; Weakly similar to !!!! ALU CLASS	5.5
	324497	AW152624	Hs.136340	ESTs	5.4
	324598	AA502659	Hs.163986	ESTs	8.8
60	324603	AW016378	Hs.292834	ESTs	23.1
	324620	AA448021	Hs.94109	EST cluster (not in UniGene)	21.2
	324727	AI610425	Hs.19597	ESTs	5
	324774	AI031771	Hs.132586	ESTs	5
	324783	AA640770	Hs.200994	EST cluster (not in UniGene)	4.1
65	324824	AI826999	Hs.224624	ESTs	6.3
	324826	AA704806	Hs.143842	ESTs	11.7
	324902	D31323	Hs.271492	ESTs	4.8

	324961	AA613792	EST cluster (not in UniGene)	13.3	
	324987	T06882	Hs.172634	ESTs	19.6
	324988	T06997	Hs.121028	EST cluster (not in UniGene)	24.5
	325146	AI054690	Hs.171176	ESTs	4.6
5	325622		CH.14_hs gj 5867000		5.2
	326213		CH.17_hs gj 5867224		8.1
	326474		CH.19_hs gj 5867405		12.7
	326816		CH.20_hs gj 6552458		9.4
	326817		CH.20_hs gj 6552458		11.7
10	327110		CH.21_hs gj 6117842		14.7
	327196		CH.01_hs gj 5867446		5.1
	327283		CH.01_hs gj 5867478		4.3
	327313		CH.01_hs gj 5867501		4.8
	327450		CH.02_hs gj 5867766		4.1
15	328059		CH.06_hs gj 6117819		6.2
	328304		CH.07_hs gj 6004478		5.4
	328492		CH.07_hs gj 5868455		7
	328857		CH.07_hs gj 6381927		5.2
	329367		CH.X_hs gj 5868842		7.6
20	329373		CH.X_hs gj 6682537		12
	329655		CH.14_p2 gj 6448516		4
	329899		CH.15_p2 gj 6563505		4
	329960		CH.16_p2 gj 5091594		7.6
	330084		CH.19_p2 gj 6015302		4
25	330384	M23263	androgen receptor (dihydrotestosterone re		5.8
	330385	AA449749	ESTs; Highly similar to secreted apoptosi		10.2
	330387	H14624	ESTs; Highly similar to secreted apoptosi		4.4
	330388	X03363	HER2 receptor tyrosine kinase (c-erbB-2;		17.7
	330409	D50692	Hs.78221	c-myc binding protein	10.1
30	330460	TIGR:HT544	Hs.73946	Endothelial Cell Growth Factor 1	5.5
	330486	M13755	Hs.833	interferon-stimulated protein; 15 kDa	67
	330494	M29696	Hs.237868	interleukin 7 receptor	6
	330500	M34423	Hs.79222	galactosidase; beta 1	13.1
	330510	M75099	Hs.227729	FK506-binding protein 2 (13kD)	29
35	330513	M81057	Hs.180884	carboxypeptidase B1 (tissue)	38.5
	330541	U22970	Hs.265827	multiple UniGene matches	7.4
	330542	U23942	Hs.226213	cytochrome P450; 51 (lanosterol 14-alpha	15
	330547	U32989	Hs.183671	tryptophan 2,3-dioxygenase	11
	330551	U39840	Hs.299867	hepatocyte nuclear factor 3; alpha	6.5
40	330562	U49082	Hs.76460	transporter protein	7.7
	330573	U62800	Hs.83393	cystatin E/M	4
	330673	D57823	Hs.321403	Sec23 (S. cerevisiae) homolog A	10.5
	330711	AA164687	Hs.177576	mannosyl (alpha-1,3-)-glycoprotein beta-1	24.3
	330814	AA015730	Hs.265398	ESTs; Weakly similar to transformation-r	44.1
45	330850	AA075298	Hs.322740	ESTs	4.4
	330874	AA127474	Hs.191157	ESTs; Weakly similar to III! ALU SUBFA	8.1
	330884	AA133457	Hs.102548	ESTs	5.2
	330912	AA195936	Hs.82719	general transcription factor IIA; 1 (37kD a	5
	330924	AA232136	Hs.159737	Homo sapiens mRNA; cDNA DKFZp434	9.1
50	330997	H55762	Hs.9302	ESTs	7.6
	331014	H98597	Hs.30340	ESTs	13.5
	331024	N32919	Hs.27931	ESTs	9.1
	331046	N66563	Hs.191358	ESTs	10.5
	331135	R61398	Hs.4197	ESTs	7.4
55	331145	R72427	Hs.129873	ESTs; Weakly similar to CYTOCHROME	41.9
	331148	R73816	Hs.17385	ESTs	4.7
	331222	T98531	Hs.173904	ESTs	4.1
	331230	W69807	Hs.16537	hypothetical protein; similar to (U06944)	4.9
	331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	15.1
60	331327	AA281076	Hs.109221	ESTs	4.8
	331337	AA287662	Hs.50495	ESTs	7.6
	331341	AA303125	Hs.23240	ESTs; Weakly similar to III! ALU SUBFA	13
	331344	AA357927	Hs.126550	ESTs	12.4
	331362	AA417956	Hs.40782	ESTs	6.5
65	331363	AA421562	Hs.91011	anterior gradient 2 (Xenopus laevis) homo	28.2
	331376	AA443802	Hs.41007	ESTs; Weakly similar to cDNA EST yk47	15.1
	331384	AA456001	Hs.93847	ESTs	7.9

	331478	N26608	Hs.40639	ESTs	7
	331526	N49967	Hs.46824	ESTs	19.8
	331533	N51517	Hs.47282	ESTs	6.5
5	331681	W65712	Hs.119571	collagen; type III; alpha 1 (Ehlers-Danlos	13.8
	331686	W88502	Hs.182258	ESTs	9.9
	331750	AA284372	Hs.111471	ESTs	5.6
	331751	AA284840	Hs.143818	ESTs	5.8
	331760	AA292721	Hs.154434	ESTs; Weakly similar to unknown [H.sap	7.4
10	331763	AA312851	Hs.96704	ESTs	7.8
	331825	AA411144	Hs.292882	ESTs	15.2
	331890	AA432166	Hs.3577	succinate dehydrogenase complex; subunit	24.3
	331952	AA454756	Hs.97837	ESTs	5
	332015	AA487910	Hs.208800	ESTs; Weakly similar to !III ALU CLASS	10.5
15	332043	AA490831	Hs.125056	ESTs	11.4
	332060	AA504779	Hs.191402	ESTs	13.6
	332071	AA598594	Hs.205293	ESTs	9.1
	332093	AA608794	Hs.112592	ESTs	8.8
	332139	AA620669	Hs.112879	EST	9
20	332219	N22508	Hs.139315	ESTs	7.1
	332225	N33213	Hs.100425	ESTs	12.2
	332246	N57927	Hs.129777	ESTs; Weakly similar to RNA POLYME	15.6
	332247	N58172	Hs.109370	ESTs	16.9
	332260	N70088	Hs.138467	ESTs	4
25	332289	N91279	Hs.109654	ESTs; Moderately similar to outer membr	8.2
	332336	T96130	Hs.137551	ESTs	7.7
	332340	W15495	Hs.129781	chromosome 21 open reading frame 5	14.1
	332347	W60326	Hs.288684	ESTs	4.4
	332362	W83640	Hs.4779	ESTs; Moderately similar to similar to AD	16.9
30	332467	AA489630	Hs.119004	KIAA0665 gene product	4.8
	332499	M12036	Hs.323910	Human tyrosine kinase-type receptor (HE	10.4
	332513	AA018182	Hs.154424	deiodinase; lodothyronine; type II	5.8
	332526	AA281753	Hs.77515	Inositol 1,4,5-triphosphate receptor; type	19
	332532	N63192	Hs.1892	EST; Highly similar to PHENYLETHAN	15.3
35	332565	AA234896	Hs.25272	E1A binding protein p300	12.3
	332607	R41791	Hs.38566	LIM domain kinase 1	11.1
	332640	AA417152	Hs.5101	protein regulator of cytokinesis 1	18.2
	332694	AA262768	Hs.243901	KIAA1067 protein	15.2
	332702	H93968	Hs.75725	transgelin 2	4.7
40	332705	TS9161	Hs.76293	thymosin; beta 10	5.5
	332749	AA479966	Hs.88251	arylsulfatase A	9.8
	332927			CH22_FGENES.38_1	17.7
	332929			CH22_FGENES.38_3	4.7
	332930			CH22_FGENES.38_4	7.4
45	332955			CH22_FGENES.48_12	5.4
	332958			CH22_FGENES.48_15	17.8
	332961			CH22_FGENES.48_18	10.6
	332983			CH22_FGENES.54_5	4.3
	333009			CH22_FGENES.61_1	5.2
50	333010			CH22_FGENES.61_2	8.1
	333013			CH22_FGENES.61_5	8.5
	333108			CH22_FGENES.79_14	5.6
	333139			CH22_FGENES.83_16	6.3
	333254			CH22_FGENES.118_2	6.8
	333305			CH22_FGENES.137_2	11.4
55	333343			CH22_FGENES.139_12	5.1
	333388			CH22_FGENES.144_3	12.7
	333456			CH22_FGENES.157_5	4.2
	333459			CH22_FGENES.157_8	7.6
	333517			CH22_FGENES.173_2	8.2
60	333585			CH22_FGENES.203_4	5
	333679			CH22_FGENES.247_6	4.3
	333743			CH22_FGENES.264_1	13.4
	333758			CH22_FGENES.268_1	4
	333767			CH22_FGENES.271_6	5.6
65	333768			CH22_FGENES.271_7	12.2
	333769			CH22_FGENES.271_8	48.3
	333795			CH22_FGENES.275_1	6.1

	333796	CH22_FGENES.275_3	6.8
	333892	CH22_FGENES.292_14	4.4
	333904	CH22_FGENES.294_2	6.5
	333905	CH22_FGENES.294_3	9.3
5	333921	CH22_FGENES.296_12	9.6
	333968	CH22_FGENES.307_4	15.9
	334102	CH22_FGENES.327_60	7.1
	334222	CH22_FGENES.360_3	6.7
	334223	CH22_FGENES.360_4	33.5
10	334264	CH22_FGENES.367_15	18.5
	334343	CH22_FGENES.375_25	6.1
	334360	CH22_FGENES.378_5	6.1
	334784	CH22_FGENES.432_9	4.8
	334789	CH22_FGENES.432_14	5.1
15	334794	CH22_FGENES.434_2	7
	334889	CH22_FGENES.452_3	12.4
	335004	CH22_FGENES.472_8	7.9
	335115	CH22_FGENES.496_2	18.8
	335287	CH22_FGENES.526_11	4.5
20	335342	CH22_FGENES.536_1	5.3
	335491	CH22_FGENES.570_23	24
	335495	CH22_FGENES.570_28	7
	335498	CH22_FGENES.571_7	12.2
	335544	CH22_FGENES.576_5	8.4
25	335610	CH22_FGENES.583_4	12.9
	335653	CH22_FGENES.590_4	6.7
	335682	CH22_FGENES.595_2	12.1
	335687	CH22_FGENES.596_2	13.9
	335755	CH22_FGENES.604_4	11.5
30	335782	CH22_FGENES.609_4	17.9
	335791	CH22_FGENES.611_7	27.3
	335809	CH22_FGENES.617_6	19.2
	335822	CH22_FGENES.619_7	19.1
	335823	CH22_FGENES.619_8	4.5
35	335824	CH22_FGENES.619_11	40.2
	335825	CH22_FGENES.619_12	34.3
	335895	CH22_FGENES.635_3	10.2
	335917	CH22_FGENES.636_13	6
	335920	CH22_FGENES.636_16	8.8
40	336035	CH22_FGENES.678_6	5.9
	336042	CH22_FGENES.679_4	5.8
	336093	CH22_FGENES.691_2	11.6
	336096	CH22_FGENES.691_5	7.6
	336150	CH22_FGENES.706_6	6.3
45	336152	CH22_FGENES.706_9	10.5
	336416	CH22_FGENES.823_38	5
	336444	CH22_FGENES.827_10	4.8
	336449	CH22_FGENES.829_6	13.6
	336471	CH22_FGENES.829_30	6.9
50	336512	CH22_FGENES.834_7	21.4
	336558	CH22_FGENES.842_3	8.2
	336560	CH22_FGENES.842_5	9
	336676	CH22_FGENES.43-4	9.4
	336959	CH22_FGENES.367-13	19
55	337968	CH22_EM:AC005500.GENSCAN.103-2	13.4
	338008	CH22_EM:AC005500.GENSCAN.127-9	15.2
	338057	CH22_EM:AC005500.GENSCAN.160-1	13.9
	338410	CH22_EM:AC005500.GENSCAN.341-6	8
	338451	CH22_EM:AC005500.GENSCAN.359-3	11.6
60	338588	CH22_EM:AC005500.GENSCAN.432-1	10.3
	338665	CH22_EM:AC005500.GENSCAN.464-2	4.8
	338689	CH22_EM:AC005500.GENSCAN.475-3	6.7
	338832	CH22_DJ246D7.GENSCAN.6-9	4.8
	338980	CH22_DA59H18.GENSCAN.2-4	5.1
65	339352	CH22_BA354I12.GENSCAN.29-7	6.9
	339373	CH22_BA232E17.GENSCAN.1-29	4.3

TABLE 13A

Table 13 A shows the accession numbers for those keys lacking unigeneID's for Table 13. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
123619	371681_1	AA602964 AA609200
103207	30635_4	X72790
103349	11052_2	X89059
110856	19346_14	AA892380 N33063 N21416 H79958 R21911 H79957
113248	328626_1	T63857 AW971220 AA493469 T63699
123169	44573_2	A1950087 N70208 R97040 N36809 A1308119 AW967677 N35320 A1251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 A1820501 A1820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA684922 SE328517 A1219788 AA884444 N92578 F13493 AA927794 A1560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 A1890387 A1950344 A1741345 A1689062 AA282915 AW102898 A1872193 A1763273 AW173586 AW150329 A1653832 A1762688 AA988777 AA488892 A1356394 AW103813 A1539642 AA642789 AA856975 AW505512 A1961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856536 AA180009 AA337499 AW951101 AA251669 AA251874 A1819225 AW205862 A1683338 A1858509 AW276905 A1633006 AA972584 AA908741 AW072629 AW513986 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 A1022058 AA780419 AA551005 W80701 AW613456 A1373032 A1564269 F00531 H83488 W37181 W78802 R66056 A1002839 R67840 AA300207 AW959581 T63226 F04005
123533	genbank_AA608751	AA608751
116480	genbank_C14088	C14088
132225	genbank_AA128980	AA128980
125154	genbank_W38419	W38419
118475	genbank_N66845	N66845
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	311935	174129_1	AA216387 T63548 AA228676
15	321050	502195_1	C05928 AW393497
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	333758	CH22_1024FG_268_1_LINK_EM:	
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336444 CH22_3864FG_827_10_LINK_D
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336471 CH22_3894FG_829_30_LINK_D

TABLE 13B

Table 13B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 13B. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
332955	Dunham, I. et al.	Plus	2508896-2508992
332958	Dunham, I. et al.	Plus	2516164-2516310
332961	Dunham, I. et al.	Plus	2521424-2521555
333139	Dunham, I. et al.	Plus	3368495-3369571
333254	Dunham, I. et al.	Plus	2521424-2521555
333305	Dunham, I. et al.	Plus	4630368-4630645
333388	Dunham, I. et al.	Plus	4913749-4913805
333517	Dunham, I. et al.	Plus	5570729-5570925
333585	Dunham, I. et al.	Plus	6234778-6234894
333679	Dunham, I. et al.	Plus	7068795-7068896
333767	Dunham, I. et al.	Plus	7694407-7694623
333768	Dunham, I. et al.	Plus	7695440-7695697
333769	Dunham, I. et al.	Plus	7696625-7696707
333795	Dunham, I. et al.	Plus	7807688-7807795
333796	Dunham, I. et al.	Plus	7808253-7808319
333892	Dunham, I. et al.	Plus	8156825-8157001
333921	Dunham, I. et al.	Plus	8380325-8380441
333958	Dunham, I. et al.	Plus	8681004-8681241
334102	Dunham, I. et al.	Plus	9995140-9995373
334284	Dunham, I. et al.	Plus	13234447-13234544
334343	Dunham, I. et al.	Plus	13655828-13656307
334794	Dunham, I. et al.	Plus	16374312-16374458
334889	Dunham, I. et al.	Plus	19286024-19286515
335287	Dunham, I. et al.	Plus	22299047-22299299
335491	Dunham, I. et al.	Plus	24128651-24128827
335495	Dunham, I. et al.	Plus	24140688-24140872
335498	Dunham, I. et al.	Plus	24172082-24172161
335653	Dunham, I. et al.	Plus	25329710-25329802
335687	Dunham, I. et al.	Plus	25445952-25446064
335809	Dunham, I. et al.	Plus	26310772-26310909
335822	Dunham, I. et al.	Plus	26364087-26364196
335823	Dunham, I. et al.	Plus	26365925-26366004
335824	Dunham, I. et al.	Plus	26376860-26376942
335825	Dunham, I. et al.	Plus	26378175-26378268
336035	Dunham, I. et al.	Plus	29016748-29017410
336093	Dunham, I. et al.	Plus	29556922-29557002
336096	Dunham, I. et al.	Plus	29578878-29579047
336444	Dunham, I. et al.	Plus	34190585-34190718
336959	Dunham, I. et al.	Plus	13233040-13233126
338008	Dunham, I. et al.	Plus	7697068-7697236
338057	Dunham, I. et al.	Plus	8526397-8526522
338410	Dunham, I. et al.	Plus	19292807-19292916
338588	Dunham, I. et al.	Plus	22896767-22896920
338665	Dunham, I. et al.	Plus	24472654-24472853
338832	Dunham, I. et al.	Plus	27775128-27775290
338980	Dunham, I. et al.	Plus	29896789-29896874
339352	Dunham, I. et al.	Plus	33544784-33545121

	332929	Dunham, I. et.al.	Minus	2020758-2020664
	332930	Dunham, I. et.al.	Minus	2022565-2022497
	332983	Dunham, I. et.al.	Minus	2631933-2631797
5	333009	Dunham, I. et.al.	Minus	2766043-2765866
	333010	Dunham, I. et.al.	Minus	2766207-2766119
	333013	Dunham, I. et.al.	Minus	2772278-2772039
	333108	Dunham, I. et.al.	Minus	3240494-3240389
	333343	Dunham, I. et.al.	Minus	4692886-4692753
	333456	Dunham, I. et.al.	Minus	2631933-2631797
10	333459	Dunham, I. et.al.	Minus	5144548-5144344
	333743	Dunham, I. et.al.	Minus	7573218-7573060
	333758	Dunham, I. et.al.	Minus	7666413-7666091
	333904	Dunham, I. et.al.	Minus	8217374-8217261
	333905	Dunham, I. et.al.	Minus	8217796-8217670
15	334222	Dunham, I. et.al.	Minus	12732417-12732289
	334223	Dunham, I. et.al.	Minus	12734365-12734269
	334360	Dunham, I. et.al.	Minus	13728850-13728751
	334784	Dunham, I. et.al.	Minus	16294548-16294360
	334789	Dunham, I. et.al.	Minus	16306095-16305996
20	335004	Dunham, I. et.al.	Minus	20581911-20581794
	335115	Dunham, I. et.al.	Minus	21388250-21388146
	335342	Dunham, I. et.al.	Minus	22597448-22597284
	335544	Dunham, I. et.al.	Minus	24650505-24650403
	335610	Dunham, I. et.al.	Minus	25068943-25068841
25	335682	Dunham, I. et.al.	Minus	25421215-25421093
	335755	Dunham, I. et.al.	Minus	25763806-25763747
	335782	Dunham, I. et.al.	Minus	25908578-25908440
	335791	Dunham, I. et.al.	Minus	25948563-25948411
	335895	Dunham, I. et.al.	Minus	26975307-26975239
30	335917	Dunham, I. et.al.	Minus	27028481-27028377
	335920	Dunham, I. et.al.	Minus	27034927-27034811
	336042	Dunham, I. et.al.	Minus	29041694-29041500
	336150	Dunham, I. et.al.	Minus	30150423-30150256
	336152	Dunham, I. et.al.	Minus	30156053-30155870
35	336416	Dunham, I. et.al.	Minus	34047408-34047311
	336449	Dunham, I. et.al.	Minus	34204707-34204577
	336471	Dunham, I. et.al.	Minus	34215091-34214978
	336512	Dunham, I. et.al.	Minus	34278373-34278275
	336558	Dunham, I. et.al.	Minus	34375825-34375698
40	336560	Dunham, I. et.al.	Minus	34376814-34376596
	336676	Dunham, I. et.al.	Minus	2022565-2022497
	337968	Dunham, I. et.al.	Minus	7095797-7095680
	338451	Dunham, I. et.al.	Minus	20174286-20174193
	338689	Dunham, I. et.al.	Minus	24893073-24892972
45	339373	Dunham, I. et.al.	Minus	33860127-33860047
	325622	5867000	Plus	69994-70075
	329655	6448516	Minus	35565-35843
	329899	6563505	Minus	111058-111783
	329980	5091594	Minus	1031-1162
50	326213	5867224	Minus	60751-60927
	326474	5867405	Plus	16995-18101
	330084	6015302	Minus	57019-59337
	326816	6552458	Plus	198354-198436
	326817	6552458	Plus	199908-200001
55	327110	6117842	Plus	94608-94785
	327196	5867446	Plus	180921-181333
	327283	5867478	Minus	567-962
	327313	5867501	Minus	89734-89838
	327450	5867766	Minus	47928-48076
60	328059	6117819	Plus	37052-37204
	328492	5868455	Minus	46094-46241
	328304	6004478	Minus	3884-3952
	328857	6381927	Minus	80557-81051
	329367	5868842	Minus	87201-87587
65	329373	6682537	Minus	38950-39301

TABLE 14: Table 2 from BRCA 001-5 US

Table 14, a subset of table 13, depicts a preferred group of genes highly upregulated in breast cancer cells.

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal breast tissue			
15	Pkey	ExAccn	UniGene ID	Unigene Title	R1
	100038	M97935		AFFX control: STAT1	16.7
	100114	D00596	Hs.82962	thymidylate synthetase	15.9
	100975	J02923	Hs.76506	lymphocyte cytosolic protein 1 (L-plastin)	30.1
20	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B; 9	37.2
	101104	L07615	Hs.169266	Human neuropeptide Y receptor Y1 (NPYY	18.3
	101143	L12723	Hs.90093	heat shock 70kD protein 4	17.4
	101332	L47276	Hs.156346	Homo sapiens (cell line HL-6) alpha topois	18.9
	101378	M13755	Hs.833	interferon-stimulated protein; 15 kDa	18.1
25	101809	M86849	Hs.323733	Homo sapiens connexin 26 (GJB2) mRNA	22.5
	102618	U85932	Hs.81071	extracellular matrix protein 1	23.2
	102721	U79241	Hs.118666	Human clone 23759 mRNA; partial cds	15
	102817	U90904	Hs.83724	Human clone 23773 mRNA sequence	15.2
	102907	X06985	Hs.202833	heme oxygenase (decycling) 1	22.7
30	102985	X17644	Hs.2707	G1 to S phase transition 1	20.6
	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin 3	17.8
	103180	X69433	Hs.5337	isocitrate dehydrogenase 2 (NADP+); mito	18.9
	103206	X72755	Hs.77367	monokine induced by gamma interferon	15.1
	103821	AA157623	Hs.198793	KIAA0750 gene product	23.3
35	104115	AA428090	Hs.26102	ESTs	28.7
	104667	AA007234	Hs.30098	ESTs	16.6
	105186	AA191512	Hs.28005	Homo sapiens mRNA; cDNA DKFZp564G	19.3
	106103	AA421104	Hs.12094	ESTs	15.4
	107151	AA621169	Hs.8687	ESTs	19
40	109415	AA227219	Hs.110826	trinucleotide repeat containing 9	20.1
	110189	H20543	Hs.6278	DKFZP586B1621 protein	16.6
	110561	H59617	Hs.5199	ESTs; Weakly similar to UBIQUITIN-CON	19.5
	110734	H98714	Hs.24131	ESTs	30.2
	110915	N46252	Hs.29724	ESTs	23.2
45	111179	N67239	Hs.10760	ESTs	37
	111357	N91023	Hs.87128	ESTs	15
	112134	R46025	Hs.7413	ESTs	17.4
	113970	W86748	Hs.8109	ESTs	15
	114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0886 protein	22
50	114292	Z40715	Hs.184641	delta-6 fatty acid desaturase	19.4
	114901	AA236276	Hs.196437	ESTs; Weakly similar to R26660_1; partial	16.9
	114965	AA250737	Hs.72472	ESTs	35.1
	115652	AA405098	Hs.38178	ESTs	16.1
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity t	33.5
55	116790	H29632	Hs.101174	microtubule-associated protein tau	22.2
	116921	H72948	Hs.821	biglycan	20.7
	117412	N26722	Hs.42645	ESTs	18.1
	120241	Z41815	Hs.65946	ESTs	15.6
	120325	AA195651	Hs.104106	ESTs	15.2
60	121596	AA416740	Hs.174104	ESTs	22.6
	123619	AA609200		ESTs	23.1
	124006	D60302	Hs.270016	ESTs	20.6
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B	25.9
	126160	N90960	Hs.265398	ESTs; Weakly similar to transformation-rel	16.4

	127677	AA916752	Hs.264190	ESTs; Highly similar to MEM3 [M.muscul	17.3
	128595	U31875	Hs.152677	short-chain alcohol dehydrogenase family m	27.1
	128717	T30617	Hs.104222	Homo sapiens mRNA; cDNA DKFZp556L	24.5
	129124	AA234530	Hs.108802	N-ethylmaleimide-sensitive factor	20.7
5	129366	H18027	Hs.184697	plexin C1	18.2
	130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyl	26.4
	130604	X03635	Hs.1657	estrogen receptor 1	39.9
	130913	W03592	Hs.21198	translocase of outer mitochondrial membra	20.9
	130944	M97935	Hs.21486	signal transducer and activator of transcript	18.8
10	131472	AA608962	Hs.27258	calcyclin binding protein	18.1
	131552	U90551	Hs.28777	H2A histone family; member L	18.8
	132180	AA405569	Hs.418	fibroblast activation protein; alpha; seprase	15.4
	132406	F09979	Hs.4774	ESTs	15
	132465	AA047896	Hs.49169	ESTs	15.4
15	132894	AA505133	Hs.279905	solute carrier family 2 (facilitated glucose t	26.4
	133294	R79723	Hs.69997	zinc finger protein 238	30.4
	133634	U24166	Hs.234279	microtubule-associated protein; RP/EB fam	15.2
	134374	D62633	Hs.8236	ESTs	15.2
	134405	J04177	Hs.82772	collagen; type XI; alpha 1	15.3
20	134470	X54942	Hs.83758	CDC28 protein kinase 2	20.3
	134495	D63477	Hs.84087	KIAA0143 protein	16.1
	134714	U89922	Hs.890	lymphotoxin beta (TNF superfamily; memb	35.7
	135237	AA454930	Hs.9691	ESTs	19.5
	301884	AA312082	Hs.105445	GDNF family receptor alpha 1	20.7
25	302276	NM_004448	Hs.323910	EST cluster (not in UniGene) with exon hit	21.6
	302290	AL117607	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N	41.4
	309177	AI951118		EST singleton (not in UniGene) with exon	24.3
	309583	AW170035		EST	64.5
	310438	AW022192	Hs.200197	ESTs	39.1
30	311166	AI821294	Hs.118599	ESTs	24.1
	312153	AA759250	Hs.153028	cytochrome b-561	27.1
	313915	AI969390	Hs.163443	ESTs	27.1
	314506	AA833655	Hs.206868	ESTs	27.8
	314558	AI873274	Hs.190721	ESTs	22.5
35	314691	AW207206	Hs.136319	ESTs	21.4
	314943	AI476797	Hs.184572	cell division cycle 2; G1 to S and G2 to M	18.4
	315196	AA972756	Hs.44898	ESTs	28.8
	316177	AI908272	Hs.293102	EST cluster (not in UniGene)	32.6
	318073	AW167087	Hs.131562	ESTs	15.7
40	318662	AI285898	Hs.294014	ESTs	16.3
	318740	NM_002543	Hs.77729	EST cluster (not in UniGene)	21.3
	318744	AI793124	Hs.144479	ESTs	35
	319668	NM_002731	Hs.87773	EST cluster (not in UniGene)	25.4
	320074	AA321166	Hs.278233	EST cluster (not in UniGene)	16.7
45	320211	AL039402	Hs.125783	DEME-6 protein	24.3
	320727	U96044	Hs.181125	EST cluster (not in UniGene)	15.3
	322818	AW043782	Hs.293616	ESTs	21
	322882	AW248508	Hs.279727	DiGeorge syndrome critical region gene 2	15.3
	324261	AL044891	Hs.269350	EST cluster (not in UniGene)	50.1
50	324432	AA464510	Hs.152812	EST cluster (not in UniGene)	16.7
	324603	AW016378	Hs.292934	ESTs	23.1
	324620	AA448021	Hs.94109	EST cluster (not in UniGene)	21.2
	324988	T06997	Hs.121028	EST cluster (not in UniGene)	24.5
	330388	X03363		HER2 receptor tyrosine kinase (c-erbB-2; E	17.7
55	330486	M13755	Hs.833	interferon-stimulated protein; 15 kDa	67
	330814	AA015730	Hs.265398	ESTs; Weakly similar to transformation-rel	44.1
	331145	R72427	Hs.129873	ESTs; Weakly similar to CYTOCHROME	41.9
	331306	AA252079	Hs.63931	dachshund (Drosophila); homolog	15.1
	331890	AA432166	Hs.3577	succinate dehydrogenase complex; subunit	24.3
60	332526	AA281753	Hs.77515	Inositol 1;4;5-triphosphate receptor; type 3	19
	332532	N63192	Hs.1892	EST; Highly similar to PHENYLETHANO	15.3
	332694	AA262768	Hs.243901	KIAA1067 protein	15.2
	332958			CH22_FGENES.48_15	17.8
	333769			CH22_FGENES.271_8	48.3
65	333968			CH22_FGENES.307_4	15.9
	334223			CH22_FGENES.360_4	33.5
	334264			CH22_FGENES.367_15	18.5

335791	CH22_FGENES.611_7	27.3
336512	CH22_FGENES.834_7	21.4
338008	CH22_EM:AC005500.GENSCAN.127-9	15.2

TABLE 14A

Table 14A shows the accession numbers for those pkeys lacking unigeneID's for Table 14. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
309583	1046029_2	AW170035
336512	CH22_3941FG_834_7_LINK_DJ	
338008	CH22_6490FG_LINK_EM:AC00	
333769	CH22_1036FG_271_8_LINK_EM	
333968	CH22_1245FG_307_4_LINK_EM	
335791	CH22_3160FG_611_7_LINK_EM	
309177	AI951118	
332958	CH22_182FG_48_15_LINK_EM:	
334223	CH22_1507FG_360_4_LINK_EM	
334264	CH22_1551FG_367_15_LINK_E	
123619	371681_1	AA602964 AA609200

TABLE 14B

- 5 **Table 14B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 14. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

- 10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 15 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
	332958	Dunham, I. et.al.	Plus	2516164-2516310
20	333769	Dunham, I. et.al.	Plus	7696625-7696707
	333968	Dunham, I. et.al.	Plus	8681004-8681241
	334264	Dunham, I. et.al.	Plus	13234447-13234544
	338008	Dunham, I. et.al.	Plus	7697066-7697236
	334223	Dunham, I. et.al.	Minus	12734365-12734269
25	335791	Dunham, I. et.al.	Minus	25948563-25948411
	336512	Dunham, I. et.al.	Minus	34278373-34278275

TABLE 15: Table 3 from BRCA 001-5 US

Table 15 shows genes downregulated in breast cancer cells.

5

Pkey: Unique Eos probeset Identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of normal breast tissue to tumor

	Pkey	ExAccn	UniGene ID	Unigene Title	R1
15	100115	D00632	Hs.172153	glutathione peroxidase 3 (plasma)	1.7
	100499	TIGR:HT1428	Hs.283108	Globin, Beta	1.5
	100502	TIGR:HT1496	Hs.169228	Adrenal-Specific Protein Pg2	2.3
20	100815	TIGR:HT4268	Hs.9739	L-Glycerol-3-Phosphate:Nad+ Oxidoreduct	1.7
	101125	L10373	Hs.82749	transmembrane 4 superfamily member 2	1.5
	101367	M12963	Hs.4	alcohol dehydrogenase 1 (class I); alpha po	2.9
	101397	M15856	Hs.180978	lipoprotein lipase	1.6
	101883	M98399	Hs.75613	CD36 antigen (collagen type I receptor; thr	1.6
	102227	U25138	Hs.93841	potassium large conductance calcium-activ	1.6
25	102857	X00129	Hs.76461	retinol-binding protein 4; interstitial	3
	103211	X73079	Hs.288579	polymeric immunoglobulin receptor	1.8
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.5
	103562	Z21966	Hs.2815	POU domain; class 6; transcription factor 1	1.8
30	104672	AA007629		glycerol-3-phosphate dehydrogenase 1 (sol	2.4
	105083	AA146619	Hs.18791	ESTs; Weakly similar to CALCIUM-BIND	1.7
	105138	AA164519	Hs.15248	ESTs	1.5
	105075	AA417915	Hs.25930	ESTs	1.5
	106870	AA487576	Hs.26530	serum deprivation response (phosphatidyls	1.6
	107099	AA609645	Hs.211598	eukaryotic translation initiation factor 4 gam	2.7
35	107616	AA004901	Hs.261164	ESTs	1.6
	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 o	1.7
	108604	AA099820	Hs.49696	ESTs	2.4
	111130	N64265	Hs.19515	yz44h12.s1 Morton Fetal Cochlea Homo sa	1.7
	111837	R36447	Hs.24453	ESTs	1.6
40	112538	R70255		ESTs	1.9
	112608	R97970	Hs.281022	EST	1.5
	113086	T40652	Hs.209100	DKFZP434C171 protein	1.9
	115740	AA418033	Hs.283559	ESTs	1.6
	115949	AA443800	Hs.43125	ESTs	2
45	115965	AA446661	Hs.173233	ESTs	2.2
	117224	N20300	Hs.218707	ESTs	1.7
	117513	N32174	Hs.44317	SRY (sex-determining region Y)-box 10	1.7
	119059	R15436	Hs.77889	Friedreich ataxia region gene X123	1.7
	119175	R71792	Hs.301002	ESTs; Weakly similar to cell death activato	2.8
50	119359	T71021	Hs.285681	ESTs; Highly similar to WS basic-helix-loop	1.9
	119798	W73386	Hs.249129	ESTs	3
	120889	AA365784	Hs.97044	ESTs	1.6
	121381	AA405747	Hs.97984	ESTs; Weakly similar to WASP-family pro	1.8
	121750	AA421184	Hs.97549	ESTs	1.5
55	122127	AA434447	Hs.106771	ESTs	2.5
	122348	AA443695	Hs.293410	ESTs	2.1
	122485	AA448300	Hs.160318	phospholemman	1.5
	123443	AA598841	Hs.167382	natriuretic peptide receptor A/guanylate cy	1.8
	123505	AA600135		ESTs; Moderately similar to IIII ALU SUB	1.5
60	125284	W94688	Hs.103253	perlepin	1.7
	126300	D81972		HUM427D08B Human fetal brain (TFujw	1.8
	126747	R72515	Hs.160318	phospholemman	1.6
	127218	AA308765	Hs.116017	ESTs; Weakly similar to KIAA0795 protei	1.5
	127357	AA452788	Hs.75432	zx39g11.r1 Scores_total_fetus_Nb2HF8_9	1.7

	127638	AA634405	Hs.122608	ESTs	1.5
	128213	AA972780	Hs.129194	ESTs; Weakly similar to Hs.129194 ALU SUBFA	1.5
	128351	A1092391	Hs.134886	ESTs	1.5
	128842	N44757	Hs.20340	ESTs	1.6
5	128870	R71403	Hs.75309	eukaryotic translation elongation factor 2	1.7
	129146	AA459944	Hs.108924	DKFZP586P1422 protein	1.5
	129285	T62068	Hs.11006	ESTs	2.1
	129331	N93465	Hs.279772	ESTs; Highly similar to CGI-38 protein [H	1.5
	130085	M62402	Hs.274313	insulin-like growth factor binding protein 6	1.7
10	130400	M25079	Hs.283108	hemoglobin; beta	1.7
	131267	AA211776	Hs.2504	myomesin 1 (skelemin) (185kD)	3.8
	131277	AA131486	Hs.23767	ESTs	1.9
	131282	M12272	Hs.4	alcohol dehydrogenase 3 (class I); gamma p	2.2
	131304	AA295848	Hs.25475	aquaporin 7	1.7
15	131810	D49487	Hs.194236	leptin (murine obesity homolog)	2.5
	132788	AA045503	Hs.56874	ESTs; Weakly similar to Homo sapiens p2	1.6
	132931	Z41452	Hs.6090	deleted in bladder cancer chromosome reg	1.5
	133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein)	2
	133314	U95367	Hs.70725	gamma-aminobutyric acid (GABA) A recep	1.5
20	133507	X74295	Hs.74369	integrin; alpha 7	1.7
	133601	S95936	Hs.284175	transferrin	2.3
	133702	N55898	Hs.75652	glutathione S-transferase M5	1.9
	134111	N79674	Hs.8022	TU3A protein	4.6
	134699	U56814	Hs.88646	deoxyribonuclease I-like 3	1.5
25	134749	L10955	Hs.89485	carbonic anhydrase IV	1.6
	135173	M72885	Hs.95910	Human GDS2 protein gene; complete cds	1.9
	300132	AW027556	Hs.156286	ESTs	1.7
	300732	A1369956	Hs.257891	ESTs	1.5
	300750	AA514805	Hs.293065	ESTs	1.8
30	301140	A1807692	Hs.129129	ESTs	1.6
	301396	AA923549	Hs.224121	ESTs	2.1
	302910	N77976	Hs.251577	hemoglobin; alpha 1	1.8
	303798	V00505	Hs.36977	hemoglobin; delta	1.6
	303831	T04868	Hs.46780	EST cluster (not in UniGene) with exon hit	1.7
35	303844	U94362	Hs.58589	glycogenin 2	1.5
	304182	H91086		EST singleton (not in UniGene) with exon	1.5
	304622	AA516384		EST singleton (not in UniGene) with exon	1.5
	304682	AA550994		EST singleton (not in UniGene) with exon	1.7
	305812	AA782347	Hs.272572	EST singleton (not in UniGene) with exon	1.5
40	306193	AA923457		EST singleton (not in UniGene) with exon	1.5
	307206	A1192534		EST singleton (not in UniGene) with exon	1.6
	307377	A1222691		EST singleton (not in UniGene) with exon	1.5
	308023	A1452732	Hs.251577	EST singleton (not in UniGene) with exon	1.9
	308359	A1612774	Hs.79372	retinoid X receptor; beta	1.5
45	309838	AW296073	Hs.255504	EST	1.5
	310403	A1720978	Hs.148006	ESTs; Moderately similar to alternatively s	1.8
	311671	AW241947	Hs.232478	ESTs	1.6
	311794	AW238092	Hs.254759	ESTs	2.1
50	312082	T79860	Hs.118180	ESTs	1.9
	312575	H25237	Hs.306814	ESTs	2.3
	313076	N49684	Hs.143040	ESTs	1.8
	313283	W32480	Hs.157099	ESTs	2.2
	313374	AW328672	Hs.132760	ESTs	1.9
	314701	A1754634	Hs.131987	ESTs	1.7
55	315391	AA759098	Hs.192007	ESTs	1.8
	315688	AA680055	Hs.264885	ESTs	1.5
	316249	AA948612	Hs.130414	ESTs	1.6
	316586	A1205077	Hs.294085	ESTs	1.7
	316890	AA837079	Hs.24647	ESTs	1.5
60	316983	A1480204	Hs.177131	ESTs	1.5
	317604	A1650625	Hs.300756	ESTs	1.6
	317951	AW206520	Hs.129621	ESTs	1.5
	319400	W26902	Hs.154085	ESTs	1.7
	320757	H22654	Hs.6382	EST cluster (not in UniGene)	1.5
65	321594	AA021402	Hs.11067	ESTs	1.7
	322102	H45589		EST cluster (not in UniGene)	1.5
	322814	A1824495	Hs.211038	ESTs	2.2

	322929	AI365585	Hs.146246	ESTs	2.3
	323831	AA335715	Hs.200299	ESTs	1.7
	324044	AL045752	Hs.22350	ESTs	1.8
	324675	AW014734	Hs.157969	ESTs	2.2
5	325272		CH.11_hs gj 5866902		1.5
	325558		CH.12_hs gj 6056302		1.6
	325656		CH.14_hs gj 6056305		1.6
	326120		CH.17_hs gj 5867194		1.5
	326139		CH.17_hs gj 5867203		1.5
10	326855		CH.20_hs gj 6552460		1.5
	327438		CH.02_hs gj 6004454		1.6
	329733		CH.14_p2 gj 6065783		1.6
	330931	F01443	Hs.284256	ESTs	4.6
	331591	N71677	Hs.42146	ESTs	1.9
15	332159	AA621393	Hs.112984	EST	1.5
	332364	W94688	Hs.103253	perilipin	2.1
	332502	H21819	Hs.14896	Homo sapiens clone 24590 mRNA sequenc	1.5
	334175		CH22_FGENES.349_10		1.5
	334347		CH22_FGENES.375_31		1.8
20	334737		CH22_FGENES.424_12		1.8
	335352		CH22_FGENES.539_5		1.5
	335639		CH22_FGENES.584_19		1.6
	336244		CH22_FGENES.746_2		1.5
	336336		CH22_FGENES.814_8		1.7
25	336865		CH22_FGENES.305-1		1.6
	337494		CH22_FGENES.799-12		1.6
	337764		CH22_EM:AC000097.GENSCAN.119-1		1.8
	337983		CH22_EM:AC005500.GENSCAN.110-1		2
	338192		CH22_EM:AC005500.GENSCAN.228-1		1.5
30	339366		CH22_BA354112.GENSCAN.34-2		1.5

TABLE 15A

Table 15A shows the accession numbers for those pkeys lacking unigeneID's for Table 15. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT number Accession

126300	250375_2	D81972 BE003132
112538	504579_1	AA908813 R70255
123505	genbank_AA600135	AA600135
104672	6735_7	AA349096 AI368018 F21390 F17759 R48772 AI421485 AI300352 H43971 AI378525 F33652 R47898 AI264177 F22289 N28263 AI276281 R48205 AI245302 AI190036 AI281050 AW242903 H42892 AA910870 AW473816 H25721 AW451438 F19647 F22375 H45809 F33447 AA774528 AA007629 H42537 C01077 F32386
322102	46708_1	H45589 H19807 AF075038 H19808 H42437
336865	CH22_4590FG_305_1_	
338192	CH22_6755FG_LINK_EM:AC00	
329733	c14_p2	
326120	c17_hs	
326139	c17_hs	
326855	c20_hs	
335352	CH22_2699FG_539_5_LINK_EM	
335639	CH22_2999FG_584_19_LINK_E	
307206	AI192534	
307377	AI222691	
337494	CH22_5727FG_799_12_	
337764	CH22_6115FG_LINK_EM:AC00	
337983	CH22_6438FG_LINK_EM:AC00	
339366	CH22_8338FG_LINK_BA35411	
325272	c11_hs	
325558	c12_hs	
325656	c14_hs	
334175	CH22_1455FG_349_10_LINK_E	
304182	H91086	
334347	CH22_1640FG_375_31_LINK_E	
327438	c_2_hs	
304622	AA516384	
334737	CH22_2049FG_424_12_LINK_E	
304682	AA550994	
336244	CH22_3642FG_746_2_LINK_DA	
306193	AA923457	
336335	CH22_3748FG_814_8_LINK_BA	

TABLE 15B

Table 15B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 15. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
334347	Dunham, I. et.al.	Plus	13663814-13663926
334737	Dunham, I. et.al.	Plus	15998517-15998685
335639	Dunham, I. et.al.	Plus	25173591-25173696
337494	Dunham, I. et.al.	Plus	33339024-33339148
334175	Dunham, I. et.al.	Minus	11668659-11668597
335352	Dunham, I. et.al.	Minus	22681512-22681384
336244	Dunham, I. et.al.	Minus	31402729-31402583
336336	Dunham, I. et.al.	Minus	33797209-33797076
336865	Dunham, I. et.al.	Minus	8622405-8622289
337764	Dunham, I. et.al.	Minus	4035640-4035446
337983	Dunham, I. et.al.	Minus	7275495-7275271
338192	Dunham, I. et.al.	Minus	13248453-13248277
339366	Dunham, I. et.al.	Minus	33647431-33647293
325272	5866902	Minus	13247-13312
325558	6056302	Plus	70930-71030
325856	6056305	Minus	78190-78707
329733	6055783	Plus	163237-163450
326120	5867194	Plus	36116-36276
326139	5867203	Minus	218901-218960
326855	6552460	Minus	111390-111463
327438	6004454	Minus	199569-199692

TABLE 16: Table 4 from BRCA 001-5 US

Table 16, a subset of table 15, depicts a preferred group of genes highly downregulated in breast cancer cells.

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UniGeneID:	UniGene number			
	UniGene Title:	UniGene gene title			
	R1:	Ratio of normal breast tissue to tumor			
15	Pkey	ExAccn	UniGene ID	UniGene Title	R1
20	100502	TIGR:HT1496	Hs.169228	Adrenal-Specific Protein Pg2	2.3
	101367	M12963	Hs.4	alcohol dehydrogenase 1 (class I); alpha	2.9
	102857	X00129	Hs.76461	retinol-binding protein 4; interstitial	3
	104672	AA007629		glycerol-3-phosphate dehydrogenase 1	2.4
	107099	AA609645	Hs.211568	eukaryotic translation initiation factor 4 gam	2.7
25	108604	AA099820	Hs.49696	ESTs	2.4
	115949	AA443800	Hs.43125	ESTs	2
	115965	AA446661	Hs.173233	ESTs	2.2
	119175	R71792	Hs.301002	ESTs; Weakly similar to cell death activator	2.8
	119798	W73386	Hs.249129	ESTs	3
30	122127	AA434447	Hs.106771	ESTs	2.5
	122348	AA443695	Hs.293410	ESTs	2.1
	129285	T62068	Hs.11006	ESTs	2.1
	131267	AA211776	Hs.2504	myomesin 1 (skelemin) (185kD)	3.8
	131282	M12272	Hs.4	alcohol dehydrogenase 3 (class I); gamma	2.2
35	131810	D49487	Hs.194236	leptin (murine obesity homolog)	2.5
	133120	X64659	Hs.65424	tetranectin (plasminogen-binding protein)	2
	133601	S95936	Hs.284176	transferrin	2.3
	134111	N79674	Hs.8022	TU3A protein	4.6
	301396	AA923549	Hs.224121	ESTs	2.1
40	311794	AW236092	Hs.254759	ESTs	2.1
	312575	H25237	Hs.306814	ESTs	2.3
	313283	W32460	Hs.157099	ESTs	2.2
	322814	AI824495	Hs.211038	ESTs	2.2
	322929	AI365585	Hs.146246	ESTs	2.3
45	324675	AW014734	Hs.157969	ESTs	2.2
	330931	F01443	Hs.284256	ESTs	4.6
	332364	W94688	Hs.103253	perilipin	2.1
	337983			CH22_EM:AC005500.GENSCAN.110-1	2

TABLE 16A

Table 16A shows the accession numbers for those pkeys lacking unigeneID's for Table 16. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT number Accession

104672 6735_7 AA349096 AI368018 F21390 F17759 R48772 AI421485 AJ300352 H43971 AI378525 F33652 R47898 AI264177 F22289 N28263
 AI276281 R48205 AI245302 AI190036 AI281050 AW242903 H42892 AA910870 AW473816 H25721 AW451438 F19647 F22375
 H45809 F33447 AA774528 AA007629 H42537 C01077 F32386

TABLE 17: Table 1 from BRCA 014 P

Table 17 shows accession numbers representing 759 sequences of breast cancer genes or fragments thereof encoding breast cancer modulating proteins. For each overexpressed gene identified, a ratio of the relative amount of expression in breast tumors versus normal breast tissue.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal breast tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
100227	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	3
100405	AW291587	Hs.82733	nidogen 2	3.2
100406	AI962080	Hs.118397	AE-binding protein 1	3.6
100420	D86983	Hs.118893	Melanoma associated gene	3.2
100911	X83300	Hs.289103	SMA4	5.2
100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	4.3
101011	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	3
101183	AA442324	Hs.795	H2A histone family, member O	3.2
101194	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	3
101329	U66042	Hs.82171	Homo sapiens clone 19187 placenta expres	4.1
101378	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	5.3
101474	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.9
101491	M25809	Hs.64173	ATPase, H+ transporting, lysosomal (vacu	4.5
101530	M29874	Hs.1360	cytochrome P450, subfamily IIB (phenobar	9
101602	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.4
101663	NM_003528	Hs.2178	H2B histone family, member Q	5.6
101758	BE019494	Hs.79217	pyrroline-5-carboxylate reductase 1	3.6
101767	M81057	Hs.180884	carboxypeptidase B1 (tissue)	12
101817	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	3.2
101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor	4.1
101878	M97815	Hs.183650	cellular retinoic acid-binding protein 2	6.5
102209	NM_002038	Hs.265827	interferon, alpha-inducible protein (clo	3
102214	U23752	Hs.32964	SRY (sex determining region Y)-box 11	3
102297	NM_001504	Hs.198252	G protein-coupled receptor 9	3.7
102299	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.7
102301	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	5.2
102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.5
102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	3.9
102591	U62325	Hs.324125	amyloid beta (A4) precursor protein-bind	4
102721	H16646	Hs.118666	hypothetical protein PP591	3.5
102739	AA363025	Hs.155572	Human clone 23801 mRNA sequence	3.2
102791	AF080229		gb:Human endogenous retrovirus K clone 1	3
102804	NM_002318	Hs.83354	lysyl oxidase-like 2	3.2
102903	M73779	Hs.250505	retinoic acid receptor, alpha	3.3
103010	X52509	Hs.161640	tyrosine aminotransferase	12.4
103042	T81656	Hs.252259	ribosomal protein S3	4.5
103117	X63578	Hs.295449	parvalbumin	3
103207	X72790		gb:Human endogenous retrovirus mRNA for	5.9
103282	BE390551	Hs.77628	steroidogenic acute regulatory protein r	3.9
103284	AI751601	Hs.8375	TNF receptor-associated factor 4	3.3
103329	X85134	Hs.72984	retinoblastoma-binding protein 5	3.1
103354	X90872	Hs.279929	gp25L2 protein	3
103385	NM_007069	Hs.37189	similar to rat HREV107	3.4
103456	AA496425	Hs.9629	papillary renal cell carcinoma (transloc	3.2

	103498	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.4
	103558	BE616547	Hs.2785	keratin 17	3.7
	103563	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK	3.2
	103612	BE336654	Hs.70937	H3 histone family, member A	4.5
5	103825	A1571835	Hs.55468	ESTs	4
	104073	AW779318	Hs.88417	ESTs	3.8
	104103	AW021102	Hs.21509	ESTs	4.3
	104115	AF183810	Hs.26102	opposite strand to trichothinophalangeal	7.6
	104168	AA461618	Hs.31704	ESTs, Weakly similar to KIAA0227 (H.sapi	3.6
10	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	4
	104181	AF173296	Hs.283740	DC6 protein	3
	104189	AB040927	Hs.301804	KIAA1494 protein	3.2
	104269	A1559444	Hs.293960	ESTs	4.3
	104307	A1929700	Hs.111680	endosulfine alpha	3.1
15	104518	H20816	Hs.112423	Homo sapiens mRNA; cDNA DKFZp58611420 (f	3.2
	104556	AV650851	Hs.96900	hypothetical protein; KIAA1830 protein	4.4
	104658	AA360954	Hs.27268	Homo sapiens cDNA: FLJ21933 fls, clone H	3.2
	104748	AA015879	Hs.33536	ESTs	3.2
	104755	T49951	Hs.9029	DKFZP434G032 protein	4.5
20	104825	AA035613	Hs.141883	ESTs	6.9
	104830	AW294092	Hs.21594	hypothetical protein MGC15754	11.1
	104865	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi	3.5
	104906	BE298684	Hs.26802	protein kinase domains containing protei	6.5
	104961	H78517	Hs.33905	ESTs	3.6
25	105038	AW503733	Hs.9414	KIAA1488 protein	4.5
	105088	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fls, clone PL	3.8
	105092	AA148982	Hs.29068	ESTs	3
	105093	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	4.8
	105304	AW134924	Hs.190325	ESTs	8.2
30	105397	AA814807	Hs.7395	hypothetical protein FLJ23182	3.1
	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.2
	105431	AA252033	Hs.242413	hypothetical protein DKFZp434K1421	4.4
	105552	AA256750	Hs.28802	centaurin-alpha 2 protein	3.2
	105595	AA279439	Hs.279763	hypothetical protein FLJ10504	3.5
35	105650	W16741	Hs.25635	HSPC003 protein	3.7
	105688	A1299139	Hs.17517	ESTs	5.5
	105808	A1133161	Hs.286131	CGI-101 protein	3.5
	105809	AW973653	Hs.20104	hypothetical protein FLJ00052	3.3
	105909	AA195191	Hs.5111	hypothetical protein FLJ20729	3.2
40	105965	AA131657	Hs.23830	ESTs	3.3
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.2
	106184	W28948	Hs.10762	ESTs	3.3
	106293	N39842	Hs.301444	KIAA1673	4.1
	106400	BE397649	Hs.94109	Homo sapiens cDNA FLJ13634 fls, clone PL	3.1
45	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.2
	106484	AA351978	Hs.4943	hepatocellular carcinoma associated prot	7.8
	106533	AL134708	Hs.145998	ESTs	3
	106614	AA648459	Hs.335951	hypothetical protein AF301222	3.8
	106636	AW958037	Hs.286	ribosomal protein L4	3.3
50	106661	AW499914	Hs.7579	hypothetical protein FLJ10402	3
	106743	BE613328	Hs.21938	hypothetical protein FLJ12492	4.2
	106844	AA485055	Hs.158213	sperm associated antigen 6	3.4
	106864	A1311928		gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	4.4
	106865	AW192535	Hs.19479	ESTs	3.6
55	106871	AW472981	Hs.321130	hypothetical protein MGC2771	4.1
	106942	AA995351	Hs.31314	retinoblastoma-binding protein 7	3.6
	106968	AF216751	Hs.26813	CDA14	5.3
	107105	AW963419	Hs.155223	stanniocalcin 2	3.4
	107158	N32849	Hs.31844	hypothetical protein FLJ12586	3.1
60	107248	AW263124	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	5.9
	107265	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	3.9
	107630	AW961576	Hs.60178	ESTs	4.6
	107710	A1955040	Hs.265398	ESTs, Weakly similar to transformation-r	3
	107890	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	3.1
65	107985	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr	4.8
	108000	A1263307	Hs.239884	H2B histone family, member L	3.3
	108217	AA058686	Hs.62588	ESTs	3.8

	108435	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3
	108591	AB033073	Hs.43857	similar to glucosamine-6-sulfatases	3.3
	108733	AA121022		gb:zn84f10.r1 Stratagene lung carcinoma	3.9
	108771	AF068290	Hs.79741	hypothetical protein FLJ10116	6.1
5	108819	AA011449	Hs.271627	ESTs	3.6
	108912	AA136674	Hs.118681	EST	3.9
	109086	AF186114	Hs.270737	tumor necrosis factor (ligand) superfamily	3.7
	109124	AK000684	Hs.183887	hypothetical protein FLJ22104	3.1
	109132	AI970536	Hs.16603	hypothetical protein FLJ13163	3.7
10	109163	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypotheti	4.5
	109277	AA196443	Hs.86043	Homo sapiens cDNA FLJ13558 fis, clone PL	3.7
	109410	AW504732	Hs.21275	hypothetical protein FLJ11011	4.6
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-in	6.4
	109514	AA234087	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	4.8
15	109581	R45584	Hs.23025	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.3
	109632	AA325138	Hs.235873	hypothetical protein FLJ22672	3
	109644	AW973964	Hs.291531	ESTs, Highly similar to 1203217A dehydro	3
	109700	F09609		gb:HSC33H092 normalized infant brain cDN	3.2
	109768	F06838	Hs.14763	ESTs	3.2
20	109807	R43646	Hs.12422	ESTs	3.8
	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	3.3
	109895	AK001680	Hs.30488	DKFZP434F091 protein	3.6
	110024	AW973152	Hs.31050	ESTs	4.2
	110581	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	5.1
25	110675	H89355	Hs.249159	adrenergic, alpha-2A-, receptor	5.3
	110707	AI239832	Hs.15517	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
	110915	BE092285	Hs.29724	hypothetical protein FLJ13187	3.7
	111139	N64683	Hs.290943	ESTs	4
	111155	N65563	Hs.191358	ESTs	3.1
30	111199	AI767435	Hs.29822	ESTs	4.5
	111336	AI457338	Hs.29894	ESTs	5.4
	111510	R07856	Hs.16355	ESTs	3.2
	111532	R08440		gb:yf19f09.s1 Soares fetal liver spleen	3.1
	111689	AA602004	Hs.23260	ESTs	3.2
35	111823	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	3.3
	111876	R38239	Hs.283246	ESTs, Weakly similar to putative p150 [H	3.1
	111892	AA421081	Hs.12388	ESTs	3.4
	111893	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	3.3
40	112125	AW379029	Hs.118338	ESTs, Weakly similar to unnamed protein	4.4
	112170	BE246743	Hs.288529	hypothetical protein FLJ22635	7.3
	112287	AB033064	Hs.334806	KIAA1238 protein	3.2
	112300	H24334	Hs.26125	ESTs	4.4
	112303	R54797		gb:yg87b07.s1 Soares infant brain 1N1B H	3.4
	112478	R65067	Hs.28664	ESTs	8.2
45	112561	AI791493	Hs.129873	ESTs, Weakly similar to A36036 cytochrom	5.6
	112631	R82040		gb:yj06b06.s1 Soares placenta Nb2HP Homo	3.9
	112637	R82331	Hs.164599	ESTs	5.4
	112657	AW844878	Hs.19769	hypothetical protein MGC4174	3.2
50	112678	AI418466	Hs.33665	ESTs	4.7
	112917	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	3.7
	113070	AB032977	Hs.6298	KIAA1151 protein	3.1
	113095	AA828380	Hs.126733	ESTs	3.4
	113117	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha	3.4
	113187	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	3.2
55	113200	T57773	Hs.10263	ESTs	3.6
	113206	BE262470	Hs.241471	RN36	6.2
	113374	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	113440	U54727	Hs.191445	ESTs	3
	113494	T91451	Hs.86538	ESTs	3.4
60	113518	AW357788	Hs.323954	postmeiotic segregation increased 2-like	3.1
	113571	AI702609	Hs.15713	hypothetical protein MGC2776	3.1
	113822	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	3.9
	113835	AI912410	Hs.27475	Homo sapiens cDNA FLJ12749 fis, clone NT	3
	113938	W81598		gb:zd88g02.s1 Soares_fetal_heart_NbHH19W	4.6
65	113947	W04768		gb:zh53d03.s1 Soares_fetal_liver_spleen_	3.1
	113970	W27249	Hs.8109	hypothetical protein FLJ21080	6.9
	114086	AA378776	Hs.288649	hypothetical protein MGC3077	4.3

	114148	AW470411	Hs.288433	neurotrophin	4.1
	114424	AW780192	Hs.267596	ESTs	3.4
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.1
	114563	AI979168	Hs.82226	glycoprotein (transmembrane) nmb	4.8
5	114965	AI733881	Hs.72472	BMP-R1B	10.1
	114995	AA769266	Hs.193657	ESTs	3.6
	115121	AI634549	Hs.88155	ESTs	3.2
	115134	AW968073	Hs.194331	ESTs, Highly similar to A55713 hoslitol	4.2
	115167	AA749209	Hs.43728	hypothetical protein	3
10	115253	BE149845	Hs.289038	hypothetical protein MGC4126	3.6
	115277	AA814100	Hs.86693	ESTs	3.9
	115327	N46436	Hs.109221	ESTs	3.4
	115354	AA281633	Hs.334827	ESTs	4.8
	115657	AA405620	Hs.55158	ESTs, Weakly similar to T29520 hypotheti	3.5
15	115676	AA953006	Hs.88143	ESTs	9.3
	115709	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.4
	115729	AA417812	Hs.38775	ESTs	4
	115787	AI126772	Hs.40479	ESTs	3.1
	115830	AW970529	Hs.86434	hypothetical protein FLJ21816	3.6
20	115835	AA521410	Hs.41371	ESTs	3.1
	115860	NM_014937	Hs.52463	KIAA0966 protein	3
	115900	AK001500	Hs.165186	hypothetical protein FLJ13852	3.2
	115935	AA354549	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3
	115948	AL042465	Hs.43445	poly(A)-specific ribonuclease (deadenyla	3.1
25	116092	AB041035	Hs.93847	NM_016931;Homo sapiens NADPH oxidase 4 (6.7
	116115	AL042355	Hs.70202	WD repeat domain 10	3.6
	116184	AW450737	Hs.128791	CGI-09 protein	3.1
	116192	AA464976	Hs.62528	ESTs, Moderately similar to A46010 X-link	3.3
	116208	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	3.2
30	116246	AF265555	Hs.250546	baculoviral IAP repeat-containing 6	3.6
	116443	AW962196	Hs.321264	LBP protein 32	4.1
	116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.1
	116726	AK001114	Hs.53913	hypothetical protein FLJ10252	8.6
	116845	AA649530	gb:ns44f05.s1 NCL_CGAP_Alv1 Homo sapiens	3.2	
35	117026	H88256	Hs.50456	ESTs, Moderately similar to ZN75_HUMAN Z	3.5
	117216	AI569804	Hs.42792	ESTs, Weakly similar to I78885 serine/th	3.1
	117296	AL133427	Hs.42506	Homo sapiens mRNA full length insert cDN	3.2
	117403	H84455	Hs.40639	ESTs	4.7
	117691	AB040959	Hs.93836	DKFZP434N014 protein	3
40	118229	AW968941	Hs.166254	hypothetical protein DKFZp566I133	3.3
	118363	AI183838	Hs.48938	hypothetical protein FLJ21802	4.3
	118416	N66028	Hs.49105	FKBP-associated protein	3.1
	118470	AW970584	Hs.291033	ESTs	3.4
	118502	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	5.2
45	118695	AK000465	Hs.50081	KIAA1199 protein	3.4
	118925	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	3.3
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	19.7
	119036	R95872	Hs.117572	chemokine binding protein 2	3.7
	119063	R16833	Hs.53105	ESTs, Moderately similar to ALU1_HUMAN A	4.1
50	119075	M10905	Hs.287820	fibronectin f	3.2
	119620	W47620	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	3.3
	119741	AF041853	Hs.43670	kinesin family member 3A	3.1
	119747	AI970797	Hs.64859	ESTs	5
	119754	AL037824	Hs.194695	ras homolog gene family, member 1	3.8
55	119905	AW449084	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	3.1
	120084	W94472	Hs.59529	ESTs, Moderately similar to ALU1_HUMAN A	8.4
	120241	AA825686	Hs.321176	ESTs, Weakly similar to S65824 reverse t	3.6
	120326	AA196300	Hs.21145	hypothetical protein RG083M05.2	3.2
	120742	AA225084	gb:nc2fd06.r1 NCL_CGAP_Pr1 Homo sapiens	3.6	
60	120870	AA357172	Hs.292581	ESTs, Moderately similar to ALU1_HUMAN A	5.8
	120885	AA365515	Hs.301872	hypothetical protein MGC4840	3
	120970	AA398118	Hs.97579	ESTs, Weakly similar to A46010 X-linked	3.7
	121054	AW976570	Hs.97387	ESTs	5.3
	121095	AA320134	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	4
65	121103	AA398936	Hs.97697	EST	3.5
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like	6.3
	121337	AW885727	Hs.301570	ESTs	4.7

	121351	AW205227	Hs.287727	hypothetical protein FLJ23132	5
	121611	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	3.6
	121643	AA640987	Hs.193767	ESTs	5.6
5	121770	NM_015902	Hs.278428	progesterin induced protein	3.4
	122125	AK000492	Hs.98806	hypothetical protein	4.1
	122338	AA443311	Hs.98998	ESTs	3
	122417	AA446965	Hs.112092	ESTs	4.7
	122513	AI767879	Hs.99214	ESTs	3.8
	122544	AW973253	Hs.292689	ESTs	3
10	122655	AA323296	Hs.97837	Homo sapiens mRNA; cDNA DKFZp547J047 (fr	5.6
	122805	AA526911	Hs.82772	collagen, type XI, alpha 1	3.2
	122851	AW205931	Hs.99598	hypothetical protein MGC5338	6.6
	123105	AA487809	Hs.166011	catenin (cadherin-associated protein), d	3
	123111	AA228776	Hs.191721	ESTs	6.9
15	123249	AA371307	Hs.125056	ESTs	3.6
	123273	AA491253	Hs.173611	Empirically selected from AFFX single pr	7
	123385	BE149685	Hs.17767	KIAA1554 protein	3.1
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.4
	123485	AI308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
20	123645	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.8
	123819	AA580082	Hs.112264	ESTs	4.7
	124012	AA352723	Hs.241471	RNB6	3.8
	124243	H69125	Hs.133525	ESTs	4.1
	124357	N22401		gb:vw37g07.s1 Morton Fetal Cochlea Homo	4.1
25	124359	N22508	Hs.139315	Homo sapiens cDNA: FLJ21479 fis, clone C	3.6
	124567	AW451645	Hs.151504	Homo sapiens cDNA FLJ11973 fis, clone HE	3.1
	124911	N34151	Hs.174195	interferon induced transmembrane protein	3.5
	124972	R41396	Hs.101774	hypothetical protein FLJ23045	4.3
	125006	BE065136	Hs.145696	splicing factor (CC1.3)	6
30	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN A	8.1
	125184	W60326	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	4.7
	125243	AW970536	Hs.105413	ESTs	3.1
	125288	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	3.3
	125304	AL359573	Hs.124940	GTP-binding protein	3
35	125330	AW880562	Hs.114574	ESTs	3
	125331	AI422996	Hs.161378	ESTs	3.2
	125685	AI924530	Hs.4943	hepatocellular carcinoma associated prot	3.2
	126257	N99638		gb:za39g11.1 Soares fetal liver spleen	4
	126474	AW975814	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	4
40	126666	AA648886	Hs.151999	ESTs	3.8
	126872	AW450979		gb:U1-H-B13-ala-a-12-0-U1.s1 NCI_CGAP_Su	3
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	3.6
	127980	AA961459	Hs.125344	ESTs	4.1
	127997	AW068311	Hs.311054	Homo sapiens mRNA full length insert cDN	3.3
45	128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.6
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	3.9
	128946	Y13153	Hs.107318	kynurenine 3-monooxygenase (kynurenine 3	3.1
	128955	AA775076	Hs.185807	Homo sapiens, Similar to PRO0478 protein	3.9
	129092	D56365	Hs.63525	poly(rC)-binding protein 2	3.3
50	129270	AA357185	Hs.109918	ras homolog gene family, member H	3.1
	129301	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	3.9
	129385	AA172106	Hs.110950	Rag C protein	6.2
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	3.4
	129629	AK000398	Hs.11747	hypothetical protein FLJ20391	3
55	129725	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.2
	130069	AI754813	Hs.146428	collagen, type V, alpha 1	5.4
	130092	X03363	Hs.323910	v-erb-b2 avian erythroblastic leukemia v	4.4
	130298	AI347487	Hs.132781	class I cytokine receptor	4.6
	130382	NM_003450	Hs.155204	zinc finger protein 174	5.6
60	130622	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisogu	3
	130703	R77776	Hs.18103	ESTs	3.8
	130881	AA809875	Hs.25933	ESTs	4.2
	130954	AB014544	Hs.21572	KIAA0644 gene product	4.7
	131095	AI399653	Hs.22917	ESTs	4.3
65	131153	H09048	Hs.23606	ESTs	3.8
	131253	R71802	Hs.24853	ESTs	3.5
	131372	AW293399	Hs.144904	nuclear receptor co-repressor 1	3.6

	131507	AI826268	Hs.27769	ESTs, Weakly similar to MCAT_HUMAN MITOC	3.2
	131587	AI695549	Hs.183868	glucuronidase, beta	3.1
	131739	AF017986	Hs.31386	secreted frizzled-related protein 2	3.2
5	131795	BE501849	Hs.32317	high-mobility group 20B	3.2
	131970	D66960	Hs.3610	KIAA0205 gene product	3.6
	131986	NM_002314	Hs.36566	LIM domain kinase 1	3.2
	132093	AA400091	Hs.39421	ESTs	3.2
	132122	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3
10	132159	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
	132333	AA192669	Hs.45032	ESTs	3.5
	132406	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f	9.2
	132482	AV660345	Hs.238126	CGI-49 protein	8.2
	132543	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.4
	132624	AA326108	Hs.33829	bHLH protein DEC2	3.2
15	132700	AA319233	Hs.5521	ESTs	4.8
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	3.6
	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2, y	3.2
	132847	T48195	Hs.58189	eukaryotic translation initiation factor	3.5
	132857	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	4.4
20	132936	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	4.8
	133130	AI128606	Hs.6557	zinc finger protein 161	3.3
	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.5
	133167	AW152840	Hs.6641	kinesin family member 5C	4.5
	133225	AW600291	Hs.6823	hypothetical protein FLJ10430	3.3
25	133274	AA085191	Hs.6949	hypothetical protein MGC11275	3
	133275	Z93241	Hs.239934	CGI-96 protein	4.5
	133287	AW797437	Hs.69771	B-factor, properdin	4.1
	133376	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	5.1
30	133462	AW675064	Hs.73875	fumarylacetoacetate hydrolase (fumarylac	3
	133740	AW162919	Hs.170160	RAB2, member RAS oncogene family-like	3.4
	133831	BE274552	Hs.76578	protein inhibitor of activated STAT3	3.9
	133976	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	6.2
	134656	BE391929	Hs.8752	transmembrane protein 4	3.1
35	134710	AM33797	Hs.8889	serine hydroxymethyltransferase 1 (solub	3
	134731	D89377	Hs.89404	nish (Drosophila) homeo box homolog 2	5.8
	134776	J05582	Hs.89603	mucln 1, transmembrane	4
	135230	AF064804	Hs.96757	suppressor of Ty (S.cerevisiae) 3 homolo	3.2
	135303	R61253	Hs.98265	KIAA1877 protein	3.3
40	135400	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.8
	135411	L10333	Hs.99947	reticulum 1	3.8
	300089	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN IIII	3.8
	300233	AW614220	Hs.189402	ESTs	4.2
	300254	AW183618	Hs.55610	solute carrier family 30 (zinc transport	9.9
45	300256	AW591433	Hs.298241	Transmembrane protease, serine 3	4.9
	300378	Z45270	Hs.235873	hypothetical protein FLJ22672	3.4
	300973	AA572949	Hs.207566	ESTs	3.5
	301111	R10799	Hs.191990	ESTs	3.8
	301341	AA887801	Hs.208229	G protein-coupled receptor	13.9
50	301548	AI091631	Hs.203845	two pore potassium channel KT3.3	4.4
	301884	AA312082	Hs.105445	GDNF family receptor alpha 1	5.7
	301936	U79745	Hs.114924	solute carrier family 16 (monocarboxylic	8.6
	301976	T97905	Hs.278346	gb:ye54c10.r1 Soares fetal liver spleen	3.9
	302001	AB020711	Hs.222399	KIAA0904 protein	7.7
55	302067	BE542706	Hs.222399	CEGP1 protein	7.3
	302094	AW749321	Hs.6786	ESTs	3.3
	302099	AL049670	Hs.137576	ribosomal protein L34 pseudogene 1	4.2
	302145	NM_003613	Hs.151407	cartilage intermediate layer protein, nu	7.9
	302235	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	5.6
	302276	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	5.4
60	302290	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	34.1
	302372	AL117405	Hs.200102	ATP-binding cassette transporter MRP8	6.7
	302378	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	4
	302384	AI678059	Hs.202676	synaptonemal complex protein 2	4.3
	302385	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	13.8
65	302680	AW192334	Hs.38218	ESTs	9.6
	302830	AI038997	Hs.132921	ESTs	5
	302857	AF282265	Hs.44836	inner centromere protein antigens (135kD	3.4

	302892	AW176909	Hs.42346	calcineurin-binding protein calcisarcin-1	3.4
	302970	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein ha	5.1
	303271	AA652687	Hs.96151	Human DNA sequence from clone RP5-1103G7	3.7
5	303289	AL121460	Hs.272673	hypothetical protein FLJ20508	4.1
	303357	AW006352	Hs.159643	ESTs, Weakly similar to T32554 hypotheti	4.2
	303540	AA355607	Hs.309490	ESTs, Weakly similar to putative WHSC1 p	4.3
	303563	AA367699	Hs.10082	potassium intermediate/small conductance	3.3
	303642	AW299459		gb:xs50d08.x1 NCI_CGAP_Kid11 Homo sapien	4.2
	303780	AI424014	Hs.18995	KIAA1304 protein	3.6
10	303797	AW629759		gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens	4.9
	303852	R53434	Hs.90207	hypothetical protein MGC11138	3.7
	304328	AA149951	Hs.62112	zinc finger protein 207	3
	304782	AA582081		gb:nn32h08.s1 NCI_CGAP_Gas1 Homo sapiens	4.1
	305913	AA876109		gb:nx24h01.s1 NCI_CGAP_GC3 Homo sapiens	3
15	305917	AA876469		gb:oe48b04.s1 NCI_CGAP_Pr25 Homo sapiens	3.1
	307010	AI140014		gb:qa68f09.x1 Soares_fetal_heart_NbHH19W	3.5
	307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	3.9
	308106	AI476803		gb:tj77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S	4.3
	308307	AI581398	Hs.172928	collagen, type I, alpha 1	4.6
20	308615	AK000142	Hs.101774	hypothetical protein FLJ23045	4.4
	309177	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	17.3
	309328	AW024348	Hs.233191	EST, Weakly similar to A27217 glucose tr	3.2
	309574	AW168083		gb:xx59g04.x1 NCI_CGAP_U14 Homo sapiens	3.1
	309583	AW170035	Hs.326736	Homo sapiens breast cancer antigen NY-BR	57.6
25	310064	AI199712	Hs.148486	ESTs, Weakly similar to 1917210A Pro/Arg	4.6
	310098	AI685841	Hs.161354	ESTs	3.6
	310438	AW022192	Hs.200197	ESTs	4.6
	310683	AI939456	Hs.160870	ESTs	3.2
	310727	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	3.6
30	310781	AI380797	Hs.158992	ESTs	10.2
	310895	AI955121	Hs.165724	N-acetylgalactosamine-4-O-sulfotransfera	3.4
	310955	AI476732	Hs.263912	ESTs	10.9
	311117	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.1
	311166	AI821005	Hs.118599	ESTs	10.8
35	311237	AA641098	Hs.208809	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	311465	AI758660	Hs.206132	ESTs	4.4
	311587	AI828254	Hs.271019	ESTs, Weakly similar to A47582 B-cell gr	5.1
	311598	AW023595	Hs.232048	ESTs	5.8
	311774	AA700870	Hs.14304	ESTs	3.3
40	311785	AI056769	Hs.133512	ESTs	3.9
	311872	R12375	Hs.194600	ESTs	3.3
	311889	AA767342	Hs.122483	ESTs, Weakly similar to PSF_HUMAN PTB-AS	3
	311913	AI358522	Hs.270188	ESTs	3
	311923	T60843	Hs.189679	ESTs	5.6
45	311935	AA216387		gb:nc16b02.s1 NCI_CGAP_Pr1 Homo sapiens	5.2
	312019	AA373630	Hs.188750	ESTs	3
	312021	AA759263	Hs.14041	ESTs	3.4
	312067	T78968	Hs.14411	ESTs	3.5
	312090	T80177	Hs.118064	similar to rat nuclear ubiquitinous casein	3.8
50	312147	AI633744	Hs.195648	ESTs, Weakly similar to I38022 hypotheti	4.4
	312153	BE261944	Hs.118625	hexokinase 1	5.2
	312168	T92251	Hs.198882	ESTs	3.3
	312182	T94344	Hs.326263	ESTs	3.3
	312187	AA700439	Hs.188490	ESTs	3.4
55	312199	AW438602	Hs.191179	ESTs	3.9
	312219	H73505	Hs.117874	ESTs	4
	312226	AA315703	Hs.199993	ESTs, Weakly similar to ALUB_HUMAN IIII	4.9
	312299	AA972712	Hs.269737	ESTs	5.7
	312544	AA516420	Hs.183526	ESTs, Weakly similar to I38022 hypotheti	6.3
60	312638	AW439195	Hs.256880	ESTs, Weakly similar to S65857 alpha-1C-	4.9
	312826	AW291545	Hs.185018	ESTs	4.9
	312837	AW292286	Hs.255058	ESTs	4.4
	312980	AA497043	Hs.115685	ESTs	3.1
	313070	AI422023	Hs.161338	ESTs	4.3
65	313079	N76497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	3.3
	313089	AF026944	Hs.293797	ESTs	5.8
	313096	AW073310	Hs.163533	Homo sapiens cDNA FLJ14142 fis, clone MA	4.5

	313126	AA746503	Hs.283313	ESTs	10
	313166	AI801098	Hs.151500	ESTs	3.5
	313197	AW979008	Hs.222487	ESTs	3.3
5	313280	AW960454	Hs.222830	ESTs	4.7
	313325	AI420611	Hs.127832	ESTs	3.4
	313328	AW449211	Hs.105445	GDNF family receptor alpha 1	12.4
	313352	AW150945	Hs.144758	ESTs	4.1
	313385	AI032087	Hs.269819	ESTs	3
	313393	AI674685	Hs.200141	ESTs	5.2
10	313417	AA741151	Hs.137323	ESTs	3.5
	313434	W92070	gb:zh48g05.r1 Soares_fetal_liver_spleen_		3.7
	313569	AI273419	Hs.135146	hypothetical protein FLJ13984	3
	313591	AA046309	gb:zf12f01.s1 Soares_fetal_heart_NbHH19W		5.6
	313615	AI540976	Hs.301997	hypothetical protein FLJ13033	3.2
15	313915	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fls, clone HE	26.3
	313975	AW175896	Hs.65114	keratin 18	3
	313979	AI535895	Hs.221024	ESTs	4.9
	313997	AV657317	Hs.288649	hypothetical protein MGC3077	3.9
	314043	AA827082	Hs.291872	ESTs	3.1
20	314078	AW129357	Hs.329700	ESTs	8.3
	314097	AA648744	Hs.269493	ESTs	6.6
	314121	AI732083	Hs.187619	ESTs	6.2
	314129	AA228366	Hs.115122	ESTs	4
25	314138	AA740616	gb:ny97f11.s1 NCLCGAP_GCB1 Homo sapiens		5.9
	314238	AA743396	Hs.189023	ESTs	3.1
	314244	AL036460	Hs.103238	ESTs	4
	314305	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fls, clone OV	8
	314306	AI697901	Hs.192425	ESTs	3.7
	314322	AA907153	Hs.190080	ESTs	3.3
30	314394	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	4.2
	314401	AI660412	Hs.234557	ESTs	3.3
	314465	AA602917	Hs.156974	ESTs	4.7
	314506	AA833855	Hs.206868	Homo sapiens cDNA FLJ14056 fls, clone HE	8.5
	314510	AI204418	Hs.190080	ESTs	4
35	314546	AW007211	Hs.16131	hypothetical protein FLJ12876	3.4
	314547	AA399272	Hs.144341	ESTs	6.7
	314558	AI873274	Hs.190721	ESTs	27.4
	314627	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	4.4
40	314646	AW979268	gb:EST391378 MAGE resequences, MAGP Homo		4.6
	314691	AW207206	Hs.136319	ESTs	20.7
	314729	AA457367	Hs.191638	ESTs	3.6
	314754	AW026761	Hs.134374	ESTs	3.6
	314814	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	4.9
45	314864	AW971198	Hs.294068	ESTs	4.3
	314881	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.7
	314882	AA828032	Hs.189076	ESTs	3.1
	314981	AW972359	Hs.293334	ESTs	3
	315006	AI538613	Hs.298241	Transmembrane protease, serine 3	10.9
50	315021	AA533447	Hs.312989	ESTs	5.3
	315051	AW292425	Hs.163484	ESTs	12.9
	315080	AA551104	Hs.189048	ESTs, Moderately similar to ALUC_HUMAN I	5.8
	315073	AW452948	Hs.257831	ESTs	4.2
	315080	AA744550	Hs.136345	ESTs	3.7
55	315175	AI025842	Hs.152530	ESTs	6
	315183	AW136134	Hs.220277	ESTs	3.9
	315193	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	4.4
	315196	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	8.2
	315198	AI741506	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.8
60	315240	R38772	Hs.172619	myelin transcription factor 1-like	3.4
	315263	AW510994	Hs.220740	ESTs	3.4
	315282	AI222165	Hs.144923	ESTs	4.9
	315296	AA876905	Hs.125286	ESTs	4
	315368	AB037745	Hs.104696	KIAA1324 protein	4.7
65	315397	AA218940	Hs.137516	fidetlin-like 1	3.1
	315489	AI378817	Hs.191847	ESTs	3.1
	315498	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.2
	315526	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypothel	4.1

	315530	AW015415	Hs.127780	ESTs	8.9
	315562	AA737415	Hs.152826	ESTs	5.5
	315634	AA837085	Hs.220585	ESTs	6.3
5	315647	AA648983	Hs.212911	ESTs	3.6
	315707	AI418055	Hs.161160	ESTs	5.1
	315772	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PL	3.1
	315850	AW270550	Hs.116957	ESTs	3.8
	315858	AA737345	Hs.294041	ESTs	5
10	315878	AA683336	Hs.189046	ESTs	3.1
	315977	AW865916	Hs.151205	ESTs	4.7
	315978	AA830893	Hs.119769	ESTs	4.1
	315995	AI217477	Hs.194591	ESTs	4.1
	316012	AA764950	Hs.119898	ESTs	7
	316042	AI469960	Hs.170698	ESTs	4.9
15	316052	AI962796	Hs.136754	ESTs	4.1
	316072	AW517524	Hs.135201	NOD2 protein	3.2
	316074	AW975114	Hs.293273	ESTs	3.8
	316100	AW203986	Hs.213003	ESTs	3.2
	316133	AI187742	Hs.125562	ESTs	3.7
20	316177	AI904982	Hs.293102	ESTs, Moderately similar to ALU1_HUMAN A	30.7
	316186	AI433540	gb:ti69g05.x1 NCI_CGAP_Kid11 Homo sapien	3.1	
	316244	AI640761	Hs.224988	ESTs	3.5
	316303	AA740994	Hs.209509	ESTs	3.8
25	316313	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypotheti	4.4
	316364	AA747807	Hs.149500	ESTs	3.2
	316580	AA938198	Hs.146123	poly(A) polymerase gamma	9.4
	316697	AW293174	Hs.252627	ESTs	4.4
	316715	AI440266	Hs.170873	ESTs, Weakly similar to T24832 hypotheti	3
30	316888	AI660898	Hs.195602	ESTs	3.2
	316869	AI954880	Hs.134604	ESTs	3.2
	316886	AA836331	Hs.134981	ESTs	4.4
	316897	AA838114	Hs.221612	ESTs	3.7
	316943	AW014875	Hs.137007	ESTs	4.5
35	317069	AI732892	Hs.190489	ESTs	5.9
	317194	AW445167	Hs.126036	ESTs	4.1
	317360	AI126252	Hs.126419	ESTs	3.5
	317404	AI806867	Hs.126594	ESTs	5.1
	317452	AA972965	Hs.135568	ESTs	6.9
40	317501	AI822034	Hs.137097	ESTs	4.6
	317674	AW284909	Hs.132208	ESTs	4.3
	317803	AW664964	Hs.128899	ESTs	6.1
	317834	X56348	Hs.287270	ret proto-oncogene (multiple endocrine n	3.1
	317850	AI681545	Hs.152982	hypothetical protein FLJ13117	3.4
	317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	9.6
45	317902	AW102941	Hs.211265	ESTs	4.1
	317916	AI565071	Hs.159983	ESTs	10.3
	318042	AW284522	Hs.149991	ESTs	3.1
	318223	AI077540	Hs.134090	ESTs	3.9
	318327	AW294013	Hs.200942	ESTs	3
50	318332	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	4.4
	318418	AF107493	Hs.118498	Homo sapiens LUCA-15 protein mRNA, splic	5.4
	318558	AW402677	Hs.146381	RNA binding motif protein, X chromosome	4.4
	318625	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	5.9
	318634	T49598	Hs.156832	ESTs	4
55	318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	7.3
	318744	AI793124	Hs.144479	ESTs	17.8
	318781	F11802	Hs.6818	ESTs	3
	319191	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
	319478	AI524124	Hs.270307	ESTs	4.6
60	319510	W88532	Hs.254562	ESTs	3.3
	319551	AA761668	gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	3.2	
	319745	T79366	Hs.108258	actin binding protein; macrophin (microf	3.3
	319834	AA071267	gb:zm61g01.r1 Stratagene fibroblast (937	6.2	
	319840	C19035	Hs.164259	ESTs	3.3
65	319977	AA534222	gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	4.3	
	320074	AA321166	Hs.278233	ESTs	3.4
	320167	AA984373	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.1

	320187	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	5.3
	320211	AL039402	Hs.125783	DEME-6 protein	9.2
	320416	AI026984	Hs.293662	ESTs	3.1
	320588	U78082	Hs.167738	RNA polymerase II transcriptional regula	3.1
5	320635	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	6.1
	320654	AI160015	Hs.118112	ESTs	3.5
	320742	AI601188	Hs.120910	ESTs	3
	320832	AA214584	Hs.290167	ESTs	3.7
	320915	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.1
10	321016	BE144167	Hs.49994	hypothetical protein similar to RNA-bind	3.3
	321107	AI732543	Hs.144151	ESTs	12.3
	321171	AI769410	Hs.221461	ESTs	3.3
	321253	AA610649	Hs.333239	ESTs	3
	321318	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	3.9
15	321642	AI432199	Hs.247084	ESTs	3
	321644	AW975944	Hs.237396	ESTs	11.7
	321683	AI471598	Hs.197531	ESTs	3.8
	321758	U29112	Hs.196151	ESTs	4.4
	321811	D80630		gb:HUM091D02B Human fetal brain (TFujiwa	3.2
20	321828	R59890	Hs.83623	nuclear receptor subfamily 1, group I, m	3.1
	321910	H67065	Hs.271530	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
	321937	AL049351	Hs.302058	Homo sapiens mRNA; cDNA DKFZp566C093 (fr	3.5
	321978	N77342	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	5
25	322035	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	19
	322136	AF075083		gb:Homo sapiens full length insert cDNA	3.6
	322258	BE265745	Hs.194359	ESTs, Weakly similar to ALUC_HUMAN IIII	3
	322296	W76326		gb:z66cd04.r1 Soares_fetal_heart_NbHH19W	4.4
	322303	AI357412	Hs.157601	ESTs	11.5
	322476	AW963372	Hs.46677	PRO2000 protein	3
30	322520	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	3
	322521	AF147347		gb:Homo sapiens full length insert cDNA	4.2
	322567	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	4
	322595	W92147	Hs.118394	ESTs	5.4
	322675	AA017666		gb:ze36h01.r1 Soares retina N2b4HR Homo	3.1
35	322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	5.2
	322818	AW043782	Hs.293616	ESTs	7.6
	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.9
	322975	C16391		gb:C16391 Clontech human aorta polyA mRNA	16.5
	323091	AI902456	Hs.210761	ESTs, Weakly similar to I38022 hypothei	4
40	323131	AK002088	Hs.270124	Homo sapiens cDNA FLJ11226 fis, clone PL	3.3
	323168	AL120862	Hs.124165	programmed cell death 9 (PDCD9)	6.3
	323244	AW675572	Hs.193620	ESTs	4.6
	323262	AL133990	Hs.190642	ESTs	10.5
	323332	AI829520		gb:wl19c06.x1 NCL_CGAP_Ut1 Homo sapiens	6.2
45	323333	AV851680	Hs.208558	ESTs	4.3
	323335	AI655499	Hs.161712	ESTs	9.2
	323645	AW445014	Hs.197746	ESTs	3.1
	323663	BE081058	Hs.243023	ESTs	4
	323693	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferri	3
50	323782	AW961560	Hs.97600	ESTs	3.2
	323817	AA410943		BMP-R1B	8.4
	323930	AL043683	Hs.8173	hypothetical protein FLJ10803	3.3
	323974	AI825204	Hs.211408	ESTs	4.5
	324001	AL044949	Hs.116298	ESTs	4.5
55	324036	AM72078	Hs.303662	ESTs	8.4
	324261	BE069341		gb:QV3-BT0381-270100-073-c08 BT0381 Homo	49.4
	324285	AA431159	Hs.122954	ESTs	3
	324296	AI524039	Hs.192524	ESTs	3
	324305	AA642007	Hs.116369	ESTs	3.3
60	324432	AA464510	Hs.152812	ESTs	16.5
	324585	AI823969	Hs.132678	ESTs	3.3
	324598	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5
	324603	AW993522	Hs.292934	ESTs	10.4
	324631	AA937116	Hs.293683	ESTs, Weakly similar to I54374 gene NF2	3.3
65	324716	BE169746	Hs.12504	likely ortholog of mouse Arkadia	3.2
	324748	AW974941	Hs.292385	ESTs, Weakly similar to I78885 serine/th	3
	324771	AA631739	Hs.335440	EST	3

	324774	AI031771	Hs.132586	ESTs	4.2	
	324823	AW516704	Hs.208726	ESTs	3.4	
	324824	AI826999	Hs.224624	ESTs	3.1	
5	324826	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	4.4	
	324961	AA613792		gb:nc97h03.s1 NCLCGAP_Pr2 Homo sapiens	3.9	
	324987	AI375572	Hs.172634	ESTs	18.8	
	324994	AI805416	Hs.213897	ESTs	3.3	
	325146	AI064690	Hs.171176	ESTs	4.2	
10	325372			Phase 2 & 3 Exons	4.4	
	325544			Phase 2 & 3 Exons	5.7	
	327075			Phase 2 & 3 Exons	3.8	
	332798			C22000007:g 12314195 emb CAB99338.1 (A	4.3	
	334223			NM_005080*:Homo sapiens X-box binding pr	26.2	
15	334447			NM_012429*:Homo sapiens SEC14 (S. cerevi	3.9	
	335809			NM_014509*:Homo sapiens kraken-like (BK1	10.1	
	335824			ENSP00000249072*:DJ22E13.1 (N-TERMINAL	20	
	338255			NM_014323*:Homo sapiens zinc finger prot	9	
	409430	R21945	Hs.166975	splicing factor, arginine/serine-rich 5	4	
20	426046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	4.6	
	432558	R97268	Hs.177269	ESTs	3.2	
	436808	AA731602	Hs.120266	ESTs	3.9	
	448569	BE382657	Hs.21486	signal transducer and activator of trans	4.1	
	453542	AW836724	Hs.339660	Homo sapiens mRNA expressed only in plac	3.7	
25		M97935		AFFX control: STAT1	3.2	
		M97935		AFFX control: STAT1	3	
		M55150		fumarylacetoacetate	3	
		M13755		interferon stimulated protein; 15 kDa	4.5	
		AI052047		ESTs	6.7	
30		AA252033		ESTs; Weakly similar to III ALU SUBFAMILY J	3.2	
		AA401739		ESTs	3.3	
		H18459		hepatocellular carcinoma associated protein;	3	
		R48744		ESTs	4.2	
		M31682		inhibin; beta B (activin AB beta polypeptide)	3	
35		AA416873		ESTs	3	
		D80240		HUM5G11A Human fetal brain (TFujiwara) Homo	4	
		R49590		ESTs	3.2	
				CH22_FGENES.678_5	16.8	
40				CH22_FGENES.619_7	12.9	
				CH22_FGENES.619_12	11.3	
				CH22_EM:AC005500.GENSCAN.127 9	9.2	
				CH22_EM:AC005500.GENSCAN.304 2	8.5	
				CH22_FGENES.271_8	8.4	
				CH22_FGENES.619_13	8	
45				CH22_FGENES.271_7	7.3	
				CH22_FGENES.617_7	7.2	
				CH.07_hs g 6004473	7.1	
				CH22_FGENES.264_1	6.8	
	X03363			HER2 receptor tyrosine kinase (c erbB 2; ERBB2; neu)	6.6	
50				CH22_FGENES.617_9	6.5	
				CH.07_hs g 5866264	5.8	
				CH.19_hs g 5867439	5.7	
				CH22_FGENES.6 3	5.3	
				CH.17_hs g 5867230	5.1	
55				CH.20_hs g 5852458	5.1	
				CH22_EM:AC005500.GENSCAN.148 22	4.7	
				CH22_FGENES.669_10	4.6	
	AA034918			KIAA1028 protein	4.6	
				CH22_FGENES.48_12	4.5	
60				CH22_FGENES.118_2	4.5	
	AF049569			ESTs	4.4	
	M13955			multiple UniGene matches	4.3	
				CH22_FGENES.619_8	4.3	
				CH22_FGENES.13 7	4.3	
65	HG4126 HT4396			Zinc Finger Protein Hzf4	4.3	
				CH22_FGENES.360_3	4.3	
				CH22_FGENES.706_9	4.3	
				CH.21_hs g 6531965	4.2	

		CH.17_hs gij5867215	4.1	
		CH22_FGENES.669_8	4.1	
	HG2614 HT2710		Collagen, Type VIII, Alpha 1	4.1
5	X83535	CH22_FGENES.48_18	4.1	
		matrix metalloproteinase 14 (membrane inserted)	4	
		CH22_FGENES.271_6	3.9	
		CH22_FGENES.617_3	3.9	
		CH22_FGENES.290_8	3.8	
10	HG4716 HT5158		Guanosine 5' Monophosphate Synthase	3.8
		CH22_FGENES.13_5	3.8	
		CH22_FGENES.13_2	3.8	
		CH.14_hs gij6682474	3.8	
		CH.02_hs gij5867750	3.8	
15	HG4677 HT5102	CH22_FGENES.617_8	3.7	
			Oncogene Ret/Ptc2, Fusion Activated	3.7
		CH22_DJ32110.GENSCAN.23_39	3.7	
		CH22_FGENES.543_20	3.7	
		CH22_EM:AC005500.GENSCAN.96_1	3.7	
20		CH22_FGENES.204_2	3.5	
		CH22_FGENES.619_4	3.5	
		CH.16_hs gij5867087	3.5	
	AA714311	EST cluster (not in UniGene)	3.4	
		CH22_EM:AC005500.GENSCAN.149_9	3.4	
25		CH22_EM:AC005500.GENSCAN.421_5	3.4	
		CH22_FGENES.13_4	3.3	
		CH.07_hs gij6004478	3.3	
		CH22_FGENES.360_1	3.3	
	HG2465 HT4871		Dna Binding Protein Ap 2, Alt. Splice 3	3.3
30		CH22_FGENES.6_2	3.3	
		CH22_C20H12.GENSCAN.16_2	3.2	
		CH22_C65E1.GENSCAN.8_1	3.2	
	AA707750	ESTs; Weakly similar to cis Golgi matrix	3.1	
		CH22_FGENES.307_4	3.1	
35		CH22_EM:AC005500.GENSCAN.248_14	3.1	
		CH.06_hs gij5902482	3.1	
		CH22_FGENES.669_5	3.1	
		CH22_DJ32110.GENSCAN.19_8	3.1	
		CH22_FGENES.527_6	3.1	
		CH22_FGENES.330_10	3.1	
40		CH22_FGENES.14_2	3.1	
	AA976074	ESTs	3	
		CH22_FGENES.226_7	3	
		CH22_FGENES.13_3	3	
45		CH22_EM:AC005500.GENSCAN.209_12	3	
		CH22_FGENES.271_3	3	

TABLE 17A

Table 17A shows the accession numbers for those pkeys lacking unigeneID's for Table 17. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT number Accession

116845	393481_1	AA649530 AA659316 H64973
103207	30635_4	X72790
126257	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
102791	37186_1	AF080229 AF080231 AF080230 AF080232 AF080233 AF080234 BE550633 AI636743 AW614951 BE467547 AI680833
		AI633818 N29986 U87592 U87593 U87590 U87591 S46404 U87587 AA463992 AW206802 AI970376 AI583718 AI672574
		N25695 AW665466 AI818326 AA126128 AI480345 AW013827 AA248638 AI214968 AA204735 AA207155 AA206262 AA204833
		AW003247 AW496808 AI080480 AI631703 AI651023 AI867418 AW818140 AA502500 AI206199 AI671282 AI352545 BE501030
		AI652535 BE465762 AA206331 AW451866 AA471086 AA206342 AA204834 AA206100 AW021661 AA332922 N66048
		AA703396 H92278 AW139734 H92683 U87589 U87595 H69001 U87594 BE466420 AI624817 BE466611 AI206344 AA574397
		AA348354 AI493192
126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359
		BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
		R82040 R70934
112631	1746257_1	AA225084 AA302713
120742	176835_1	AI311928 AA936030 T51931 AA609816 AA487195 AA664207
105864	324239_1	
109700	genbank_F09609	F09609
111532	genbank_R08440	R08440
113938	genbank_W81598	W81598
113947	genbank_W84768	W84768
124357	genbank_N22401	N22401
108733	504187_1	AA121022 AA126422
112303	genbank_R54797	R54797
322136	46802_1	AF075083 H52291 H52528
322295	47334_1	W76326 AF086341 W72300
321811	1527481_1	D80630 D80896 D80895
314648	293660_1	AW979268 AA878419 AA431342 AA431628
322520	38916_1	T55958 T57205 AF147346
322521	38917_1	AF147347 T55426 T55503
322675	86787_1	AA017656 AA017374 AA019761
323332	179142_1	AI829520 AI791832 AA228414 AI791823 AA229211 AA229315
316186	425440_1	AI433540 AA728984 AA804981
322975	1510563_1	C16391 C16413
324261	273265_1	BE069341 AW748403 AL044891 AI908240 AA393080
323817	233566_1	AA410943 AW948953 AA334202 AA332882
301976	128835_1	T97905 AA101672
324961	376239_1	AA613792 AW182329 T05304 AW858385
303642	284260_1	AW299459 AA417112
303797	386364_1	AW629759 AW749955 AA633408 AI851005
319551	357371_1	AA761668 AA573621 R92814 R09670
311935	174129_1	AA216387 T63548 AA228676
319834	112523_1	AA071267 T65940 T64515 AA071334
319977	345246_1	AA534222 AA632632 T81234
314138	179960_1	AA740616 AA654854 AA229923
313591	103087_1	AA046309 AI263500 AA046397

308106 AI478803
338255 CH22_6856FG_LINK_EM:AC00
335809 CH22_3181FG_617_6_LINK_EM
5 335824 CH22_3197FG_619_11_LINK_E
307010 AI140014
307041 AI144243
305913 AA876109
305917 AA876489
309574 AW168083
10 325372 c12_hs
325544 c12_hs
332798 CH22_14FG_6_5_LINK_C4G1.G
334223 CH22_1507FG_360_4_LINK_EM
327075 c21_hs
15 334447 CH22_1746FG_387_7_LINK_EM
304782 AA582081
313434 441798_1 W92070 AW019952 W92053

TABLE 17B

Table 17B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 17. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
334447	Dunham, I. et al.	Plus	14308764-14308824
335609	Dunham, I. et al.	Plus	26310772-26310909
335824	Dunham, I. et al.	Plus	26376860-26376942
332798	Dunham, I. et al.	Minus	232147-231974
334223	Dunham, I. et al.	Minus	12734365-12734269
338255	Dunham, I. et al.	Minus	15242294-15242231
325372	5866920	Minus	1117061-1117304
325544	6682452	Plus	171228-171286
327075	6531965	Plus	4041318-4041431

TABLE 18: Table 2 from BRCA 014 P

Table 18 shows genes with atleast five times the expression in breast tumor tissue than is expressed in normal body tissues.

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal body tissue			
15	Pkey	ExAccn	UnigeneID	Unigene Title	R1
20	101378	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	5.3
	101530	M29874	Hs.1380	cytochrome P450, subfamily IIB (phenobar	9
	101767	M81057	Hs.180884	carboxypeptidase B1 (tissue)	12
	101878	M97815	Hs.183650	cellular retinoic acid-binding protein 2	6.5
	103010	X52509	Hs.161640	tyrosine aminotransferase	12.4
25	104115	AF183810	Hs.26102	opposite strand to trichorhinophalangeal	7.6
	104825	AA035613	Hs.141883	ESTs	6.9
	107105	AW963419	Hs.155223	stanniocalcin 2	5.3
	108819	AA011449	Hs.271627	ESTs	6.1
	112287	AB033064	Hs.334806	KIAA1238 protein	7.3
30	112561	AI791493	Hs.129873	ESTs, Weakly similar to A36036 cytochrom	8.2
	112637	R82331	Hs.164589	ESTs	5.4
	113206	BE262470	Hs.241471	RNB6	6.2
	113970	W27249	Hs.8169	hypothetical protein FLJ21080	6.9
	114935	AI733881	Hs.72472	BMP-R1B	10.1
35	118925	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	19.7
	119905	AW449064	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	8.4
	121611	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	5.6
	129301	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	6.2
	133976	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	6.2
40	134731	D89377	Hs.89404	msh (Drosophila) homeo box homolog 2	5.8
	300254	AW183618	Hs.55610	solute carrier family 30 (zinc transport	9.9
	301884	AA312082	Hs.105445	GNDF family receptor alpha 1	5.7
	302001	AB020711	Hs.278346	KIAA0904 protein	7.7
	302067	BE542706	Hs.222399	CEGP1 protein	7.3
45	302276	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	5.4
	302290	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0783 (f34.1	13.1
	302372	AL117406	Hs.200102	ATP-binding cassette transporter MRP8	6.7
	302385	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	13.8
	309177	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	17.3
50	309583	AW170035	Hs.326736	Homo sapiens breast cancer antigen NY-BR	57.6
	310781	AI380797	Hs.158992	ESTs	10.2
	311166	AI821005	Hs.118599	ESTs	10.8
	311935	AA216387		gb:nc16b02.s1 NCL_CGAP_Pr1 Homo sapiens	5.2
	312153	BE261844	Hs.118625	hexokinase 1	5.2
55	313328	AW449211	Hs.105445	GNDF family receptor alpha 1	12.4
	313915	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fls, clone HE	26.3
	314097	AA648744	Hs.269493	ESTs	6.6
	314138	AA740616		gb:ny97f11.s1 NCL_CGAP_GCB1 Homo sapiens	5.9
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fls, clone HE	8.5
60	314558	AI873274	Hs.190721	ESTs	27.4
	314691	AW207206	Hs.136319	ESTs	20.7
	315006	AI538613	Hs.298241	Transmembrane protease, serine 3	10.9
	315021	AA533447	Hs.312989	ESTs	5.3
	315051	AW292425	Hs.163484	ESTs	12.9
	315060	AA551104	Hs.189048	ESTs, Moderately similar to ALUC_HUMAN I	5.8

	315196	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	8.2
	315530	AW015415	Hs.127780	ESTs	8.9
	315634	AA837085	Hs.220585	ESTs	6.3
5	316012	AA764950	Hs.119898	ESTs	7
	316177	AI904982	Hs.293102	ESTs, Moderately similar to ALU1_HUMAN A	30.7
	316580	AA938198	Hs.148123	poly(A) polymerase gamma	9.4
	317803	AW664984	Hs.128899	ESTs	6.1
	317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	9.6
10	318740	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	7.3
	318744	AI793124	Hs.144479	ESTs	17.8
	320211	AL039402	Hs.125783	DEME-6 protein	9.2
	321107	AI732643	Hs.144151	ESTs	12.3
	321644	AW975944	Hs.237396	ESTs	11.7
15	321978	N77342	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	5
	322035	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	19
	322766	AW068805	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	5.2
	322818	AW043782	Hs.293616	ESTs	7.6
	322975	C16391		gb:C16391 Clontech human aorta polyA mRN	16.5
20	323262	AL133990	Hs.190642	ESTs	10.5
	323332	AI829520		gb:wl19c06.x1 NCL_CGAP_U11 Homo sapiens	6.2
	323817	AA410943		BMP-R1B	8.4
	324261	BE069341		gb:QV3-BT0381-270100-073-c08 BT0381 Homo	49.4
	324432	AA464510	Hs.152812	ESTs	16.5
25	324598	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5
	324603	AW993522	Hs.292934	ESTs	10.4
	324987	AI375572	Hs.172634	ESTs	18.8
	325544			Phase 2 & 3 Exons	5.7
	330388		Hs.46	HER2 receptor tyrosine kinase (c-erb-b2,	6.6
30	334223			NM_005080*:Homo sapiens X-box binding pr	26.2
	335809			NM_014509*:Homo sapiens kraken-like (BK1	10.1
	335824			ENSP00000249072*:DJ222E13.1 (N-TERMINAL	20
	AI052047			ESTs; Weakly similar to CYTOCHROME P450	6.7
	R72427			CH22_EM:AC005500.GENSCAN.127 9	5.5
35				CH22_FGENES.619_13	9.2
				CH22_FGENES.617_9	8
				CH22_FGENES.271_7	6.5
				CH22_FGENES.619_7	7.3
				CH22_FGENES.271_8	12.9
				CH22_FGENES.619_12	8.4
40				CH22_EM:AC005500.GENSCAN.304 2	11.3
				CH.07_hs g16004473	8.5
				CH22_FGENES.617_7	7.1
				CH22_FGENES.678_5	7.2
				CH22_FGENES.678_5	16.8

TABLE 18A

Table 18A shows the accession numbers for those pkeys lacking unigeneID's for Table 18. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
323332	179142_1	AI829520 AI791832 AA228414 AI791823 AA229211 AA229315
322975	1510563_1	C16391 C16413
324261	273265_1	BE069341 AW748403 AL044891 AI908240 AA393080
323817	233566_1	AA410943 AW948953 AA334202 AA332882
311935	174129_1	AA216387 T63548 AA228676
314138	179980_1	AA740616 AA654854 AA229923
335809	CH22_3181FG_617_6_LINK_EM	
335824	CH22_3197FG_619_11_LINK_E	
325544	c12_hs	
334223	CH22_1507FG_360_4_LINK_EM	

TABLE 18B

5 **Table 18B** shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 18. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 **Pkey:** Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
15 **Nt_position:** Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
20	335809	Dunham, I. et al.	Plus	26310772-26310909
	335824	Dunham, I. et al.	Plus	26376660-26376942
	334223	Dunham, I. et al.	Minus	12734365-12734269
	325544	6682452	Plus	171228-171286

**TABLE 19: 1045 GENES UP-REGULATED IN BREAST CANCER
COMPARED TO NORMAL ADULT TISSUES**

5 **Table 19** shows 1045 genes up-regulated in breast cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" breast cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" breast cancer level was set to the 90th percentile value. The "average" normal adult tissue level was set to the 90th percentile value amongst 144 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the 144 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

15 Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
20 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigeneID	UnigeneTitle	R1
	408591	AF015224	Hs.46452	mammaglobin 1	137.6
25	406964	M21305		gb:Human alpha satellite and satellite 3	71.0
	400291	AA401369	Hs.190721	ESTs	68.4
	407277	AW170035	Hs.326736	Homo sapiens breast cancer antigen NY-BR	54.2
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	46.4
	426878	BE069341		gb:QV3-BT0381-270100-073-c08 BT0381 Homo	44.8
30	400292	AA250737	Hs.72472	BMP-R1B	37.4
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	32.9
	408045	AW138959	Hs.245123	ESTs	31.9
	407178	AA195651	Hs.104106	ESTs	30.4
	407377	C16391		gb:C16391 Clontech human aorta polyA mRN	27.7
35	450705	U90304	Hs.25351	Iroquois homeobox protein 5	24.8
	407212	AA412108	Hs.269350	ESTs	22.0
	428648	NM_000230	Hs.194236	lepin (murine obesity homolog)	21.9
	404561			trichorhinophalangeal syndrome I (TRPS1)	21.8
	407980	AA046309		gb:zf12f01.s1 Soares_fetal_heart_NbHH19W	19.8
40	447350	AI375572	Hs.172634	ESTs	17.3
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	16.6
	422109	S73265	Hs.1473	gastrin-releasing peptide	16.5
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	16.0
	453160	AI263307	Hs.239884	H2B histone family, member L	15.8
45	420813	X51501	Hs.99949	prolactin-induced protein	15.8
	415989	AI267700	Hs.317584	ESTs	15.5
	422505	AL120862	Hs.124165	programmed cell death 9 (PDCD9)	14.8
	424399	AI905687	Hs.2533	aldehyde dehydrogenase 9 family, member	14.5
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	13.7
50	429441	AJ224172	Hs.204096	lipophilin B (uterglobin family member)	13.6
	431474	AL133990	Hs.190642	ESTs	13.5
	448595	AB014544	Hs.21572	KIAA0644 gene product	13.0
	427217	AA399272	Hs.144341	ESTs	12.8
	402578			C1001134:gl 2117372 pir 65981 fatty ac	12.6
55	422805	AA436989	Hs.121017	H2A histone family, member A	12.2
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nu	12.0
	456207	AA193450		gb:zr40e07.r1 Soares_NhHMPu_S1 Homo sapi	11.9
	424086	AI351010	Hs.102267	lysyl oxidase	11.9
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	11.5

	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	11.5
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	11.5
	407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	11.4
	434377	AW137148	Hs.308593	Homo sapiens cDNA FLJ11382 fis, clone HE	11.3
5	448390	AL035414	Hs.21068	hypothetical protein	11.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	11.0
	421037	AI684808	Hs.197653	programmed cell death 9 (PDCD9)	10.9
	452461	N78223	Hs.108106	transcription factor	10.7
	443348	AW873596	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	10.6
10	421155	H87879	Hs.102267	lysyl oxidase	10.5
	402606		NM_024626	Homo sapiens hypothetical prot	10.4
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	10.4
	447268	AI370413	Hs.36563	hypothetical protein FLJ22418	10.3
	447033	AI357412	Hs.157601	ESTs	10.2
15	400295	W72838	Hs.2533	aldehyde dehydrogenase 9 family, member	10.1
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	10.1
	432441	AW292425	Hs.163484	ESTs	9.9
	427365	AI873274	Hs.190721	ESTs	9.9
	438950	H23789	Hs.144530	EST	9.8
20	422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	9.7
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	9.7
	411869	W20027	Hs.23439	ESTs	9.6
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	9.6
	445730	AI624342	Hs.170042	ESTs	9.5
25	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	9.3
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	9.2
	432596	AJ224741	Hs.278461	matrilin 3	9.1
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564C1278	9.1
	449448	D60730	Hs.57471	ESTs	9.1
30	423945	AA410943		gb:z32h03.r1 Soares ovary tumor NbHOT H	9.1
	406348			Target Exon	9.0
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	9.0
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	9.0
	433365	AF026944	Hs.293797	ESTs	8.8
35	405654	NA		C12001521:gil7513934 pir JT31081 cca3 pr	8.8
	418601	AA279490	Hs.86368	calnegin	8.8
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	8.7
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	8.5
	409041	AB033025	Hs.50081	KIAA1199 protein	8.4
40	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	8.3
	451561	N52812	Hs.177403	ESTs	8.2
	424001	W67883	Hs.137476	paternally expressed 10	8.2
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	8.1
	423887	AL080207	Hs.134585	DKFZP434G232 protein	8.1
45	405095	NA		Target Exon	8.1
	419296	AA236115	Hs.120785	ESTs	8.0
	447164	AF026941	Hs.17518	Homo sapiens clg5 mRNA, partial sequence	8.0
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	8.0
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	8.0
50	415385	R17798	Hs.7535	COBW-like protein	7.9
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	7.9
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	7.9
	406687	M31126	Hs.272620	matrix metalloproteinase 11 (MMP11; stro	7.8
	400285	NA		Eos Control	7.7
55	437207	T27503	Hs.15929	hypothetical protein FLJ12910	7.6
	427119	AW880562	Hs.114574	ESTs	7.5
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	7.5
	433426	H69125	Hs.133525	ESTs	7.5
	411078	AI222020	Hs.182364	CocoaCrisp	7.4
60	426214	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	7.4
	447475	AI380797	Hs.158992	ESTs	7.3
	415263	AA948033	Hs.130853	ESTs	7.2
	439569	AW602166	Hs.222399	CEGP1 protein	7.2
	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	7.1
65	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	7.0
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	6.9
	445885	AI734009	Hs.127699	KIAA1603 protein	6.9

	429432	AI678059	Hs.202676	synaptonemal complex protein 2	6.9
	410781	AI375672	Hs.165028	ESTs	6.9
	443788	AI732643	Hs.144151	ESTs	6.9
	421373	AA808229	Hs.167771	ESTs	6.8
5	451398	AI793124	Hs.144479	ESTs	6.8
	404253		NM_021058*	Homo sapiens H2B histone fami	6.8
	441098	AI015591	Hs.131004	ESTs, Weakly similar to T17227 hypotheti	6.7
	426215	AW963419	Hs.155223	stanniocalcin 2	6.6
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (CX	6.6
10	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	6.6
	411111	AW818127		gb:CM1-ST0277-061299-059-b07 ST0277 Homo	6.6
	434988	AI418055	Hs.161160	ESTs	6.6
	442580	AI733682	Hs.130239	ESTs	6.6
	449611	AI970394	Hs.197075	ESTs	6.6
15	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	6.5
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	6.5
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	6.5
	400301	X03635	Hs.1657	estrogen receptor 1	6.5
	427356	AW023482	Hs.97849	ESTs	6.5
20	425704	U79293	Hs.159284	Human clone 23948 mRNA sequence	6.4
	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	6.4
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	6.4
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.4
	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	6.2
25	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	6.1
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	6.1
	453331	AI240865	Hs.8895	ESTs	6.1
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (MMP1; inters	6.0
	441233	AA972965	Hs.135568	ESTs	6.0
30	418092	R45154	Hs.106604	ESTs	6.0
	430044	AA464510	Hs.152812	ESTs	5.9
	432837	AA310693	Hs.87329	HSPC072 protein	5.9
	433285	AW975944	Hs.237396	ESTs	5.9
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	5.9
35	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	5.9
	410785	AW803341		gb:HL2-UM0079-090300-050-D03 UM0079 Homo	5.9
	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	5.9
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.8
	459371	R20991		gb:yg06h01.r1 Soares infant brain 1N1B H	5.8
40	411284	N28519	Hs.135191	ESTs, Weakly similar to unnamed protein	5.8
	453511	AL031224	Hs.33102	transcription factor AP-2 beta (activati	5.8
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	5.7
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	5.7
	415539	AI733981	Hs.72472	BMP-R1B	5.6
45	438199	AW016531	Hs.122147	ESTs	5.6
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	5.5
	430019	AA463893	Hs.220933	ESTs	5.5
	439809	R41393	Hs.101774	hypothetical protein FLJ23045	5.5
	423811	AW299598	Hs.50895	homeo box C4	5.4
50	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	5.4
	439138	AI742605	Hs.193696	ESTs	5.4
	453931	AL121278	Hs.25144	ESTs	5.4
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	5.4
	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypotheti	5.4
55	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	5.4
	425235	AW067800	Hs.155223	stanniocalcin 2	5.3
	421464	AA291553	Hs.190086	ESTs	5.3
	450735	AW970060		gb:EST382140 MAGE resequences, MAGK Homo	5.3
	428065	AA421081	Hs.12388	ESTs	5.3
60	452838	U65011	Hs.30743	preferentially expressed antigen in mela	5.3
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	5.3
	456938	X52509	Hs.161640	tyrosine aminotransferase	5.3
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (COM	5.2
	438167	R28363	Hs.24286	ESTs	5.2
65	433330	AW207084	Hs.132816	hypothetical protein MGC14801	5.2
	449765	N92293	Hs.208832	ESTs, Moderately similar to ALU8_HUMAN A	5.2
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	5.2

	400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	5.2
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	5.2
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	5.2
	428771	AB028992	Hs.193143	KIAA1069 protein	5.2
5	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.2
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	5.2
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	5.1
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	5.1
	431023	AI283133	Hs.297420	ESTs	5.1
10	427666	AI791495	Hs.180142	calmodulin-like skin protein	5.1
	427718	AI798680	Hs.25933	ESTs	5.1
	434531	AA642007	Hs.116369	ESTs	5.1
	429220	AW207206	Hs.136319	ESTs	5.1
	405494	NA		C2001837*gi12697903 db BAB21770.1 (A	5.1
15	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypotheti	5.1
	444910	AI201849		gb:qs76g04.x1 NCL CGAP_Pr28 Homo sapiens	5.1
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	5.0
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	5.0
	450603	R43646	Hs.12422	ESTs	5.0
20	416575	W02414	Hs.38383	ESTs	5.0
	438504	AW665281	Hs.224625	ESTs	5.0
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	5.0
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	5.0
	420077	AW512260	Hs.87767	ESTs	4.9
25	450480	X82125	Hs.25040	zinc finger protein 239	4.9
	437637	AJ003029	Hs.65792	syntrophin, gamma 2	4.9
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	4.9
	418836	AI655499	Hs.161712	ESTs	4.8
	442441	AI820662	Hs.129598	ESTs	4.8
30	435635	AF220050	Hs.181385	uncharacterized hematopoietic stem/proge	4.8
	400286	NA		C16000922:gi7499103 pir T20903 hypothe	4.8
	407508	U71600		gb:Human zinc finger protein zfp31 (zf31	4.8
	420026	AI831190	Hs.166676	ESTs	4.8
	441377	BE218239	Hs.202656	ESTs	4.8
35	457726	AI217477	Hs.194591	ESTs	4.8
	412785	AW997556	Hs.78521	KIAA1717 protein	4.8
	428368	BE440042	Hs.83325	matrix metalloproteinase 3 (stromelysin	4.7
	436025	AI349764	Hs.217081	ESTs	4.7
	409110	AA191493	Hs.48776	niban protein	4.7
40	400284	NA		estrogen receptor 1	4.7
	410102	AW246508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	4.7
	407819	R42185	Hs.274803	ESTs	4.7
	430483	BE062109	Hs.241551	chloride channel, calcium activated, fam	4.7
	422895	AW961489	Hs.154116	ESTs	4.7
45	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	4.7
	427427	AF077345	Hs.177936	ESTs	4.6
	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha	4.6
	454074	R63503	Hs.28419	ESTs	4.6
	405718			C4000799*gi6330365 db BAA86508.1 (AB	4.6
50	444649	AW207523	Hs.197628	ESTs	4.6
	429431	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	4.6
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	4.6
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	4.6
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	4.6
55	454307	AW855717		gb:RC1-CT0279-081299-013-b01 CT0279 Homo	4.6
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	4.6
	438180	AA808189	Hs.272151	ESTs	4.6
	451340	AW936273		gb:QV0-DT0020-030200-107-g97 DT0020 Homo	4.6
	458711	AL036877	Hs.282878	ESTs	4.6
60	457430	AA514660	Hs.128443	ESTs	4.6
	416030	H15261	Hs.21948	ESTs	4.6
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	4.6
	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6 (EGFL6)	4.5
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	4.5
65	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	4.5
	423833	AW503329		gb:U1-HF-BN0-akx-e-02-0-U1.r1 NIH_MGC_50	4.5
	405747	AI925153	Hs.217493	annexin A2	4.5

	412102	H56435		gb:yq98e09.r1 Soares fetal liver spleen	4.5
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	4.5
	411050	AW814902		gb:MR1-ST0206-120400-022-008 ST0206 Homo	4.5
5	401418	NA		C14000338*:gij7459502 pir S74665 outer	4.5
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	4.5
	436211	AK001561	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.4
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	4.4
	424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypotheti	4.4
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	4.4
10	442117	AW664964	Hs.128899	ESTs	4.4
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	4.4
	432731	R31178	Hs.287820	fibronectin 1	4.4
	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	4.4
	405196	NA		C2000662*:gij7512792 pir T12482 hypothe	4.4
15	430217	N47863	Hs.336901	ribosomal protein S24	4.4
	401793			C17001545:gij5360127 gb AAD42882.1 AF155	4.4
	415747	AA381209		gb:EST94257 Activated T-cells 1 Homo sap	4.4
	423679	AB007975	Hs.131454	KIAA0506 protein	4.4
	400238	NA		C19000274*:gij12741327 ref XP_008833.2	4.4
20	425627	AF019612	Hs.297007	membrane-bound transcription factor prot	4.4
	400608			C10001899:gij7508633 pir T25392 hypothe	4.4
	458634	AV657310	Hs.282898	ESTs	4.3
	407771	AL138272	Hs.62713	ESTs	4.3
25	405906	NA		Target Exon	4.3
	405925	NA		Target Exon	4.3
	439382	BE247684	Hs.103070	ESTs	4.3
	445263	H57646	Hs.42586	KIAA1560 protein	4.3
	407162	N63855	Hs.142634	zinc finger protein	4.3
30	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	4.3
	454359	N71277		gb:za38e03.s1 Soares fetal liver spleen	4.3
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	4.2
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.2
	421451	AA291377	Hs.50831	ESTs	4.2
35	452864	AA033714	Hs.287629	hypothetical protein FLJ14260	4.2
	409757	NM_001898	Hs.123114	cystatin SN	4.2
	413043	BE158766		gb:IL2-HT0397-071299-024-F02 HT0397 Homo	4.2
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	4.2
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	4.2
40	408380	AF123050	Hs.44532	diubiquitin	4.2
	406992	S82472		gb:beta-pol-DNA polymerase beta (exon a	4.2
	404285	NA		C6001909:gij704441 dbj BAA18909.1 D298	4.2
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stro	4.2
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	4.2
45	446163	AA026880	Hs.25252	prolactin receptor	4.2
	421147	AW592167	Hs.293299	ESTs	4.2
	426451	AI908185	Hs.169946	GATA-binding protein 3 (T-cell receptor	4.2
	415227	AW821113	Hs.72402	ESTs	4.2
	452176	AA024538	Hs.282990	Human DNA sequence from clone RP1-26H20	4.2
50	452862	AW378055	Hs.8687	ESTs	4.2
	443646	AI085198	Hs.164226	ESTs	4.2
	425523	AB007948	Hs.158244	KIAA0479 protein	4.1
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.1
	430009	AA894564	Hs.22242	ESTs	4.1
55	434469	AA634806		gb:ab28c02.r1 Stratagene lung (937210) H	4.1
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	4.1
	450229	R18717	Hs.8929	hypothetical protein FLJ11362	4.1
	455700	BE068115		gb:CM1-BT0368-061299-060-g07 BT0368 Homo	4.1
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	4.1
60	438885	AI686558	Hs.184987	ESTs	4.1
	401451			NM_004496*:Homo sapiens hepatocyte nucle	4.1
	431676	AI685464		gb:tt88604.x1 NCI_CGAP_Pr28 Homo sapiens	4.1
	409092	AI735283	Hs.172608	ESTs	4.1
	429270	W60379	Hs.57773	ESTs	4.1
	443903	AI220547	Hs.135223	ESTs	4.1
65	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	4.1
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.1
	432912	BE007371	Hs.200313	ESTs	4.1

	403585		Target Exon	4.1
	438295	AI394151	Hs.37932 ESTs	4.1
	420380	AA640891	Hs.102406 ESTs	4.1
	431118	BE264901	Hs.250502 carbonic anhydrase VIII	4.1
5	416182	NM_004354	Hs.79069 cyclin G2	4.1
	418994	AA296520	Hs.89546 selectin E (endothelial adhesion molecu	4.1
	400555		Target Exon	4.1
	410079	U94362	Hs.58589 glycogenin 2	4.0
	427674	NM_003528	Hs.2178 H2B histone family, member Q	4.0
10	427131	AA448460	Hs.112017 GE36 gene	4.0
	439759	AL359055	Hs.67709 Homo sapiens mRNA full length insert cDN	4.0
	429353	AL117406	Hs.200102 ATP-binding cassette transporter MRP8	4.0
	421296	NM_002666	Hs.103253 perilipin	4.0
	418819	AA228776	Hs.191721 ESTs	4.0
15	424188	AW954552	Hs.142634 zinc finger protein	4.0
	455431	AW938484	gb:CM0-DT0057-290200-253-d06 DT0057 Homo	4.0
	404142	NA	Target Exon	4.0
	441143	AI027604	Hs.159650 ESTs	4.0
	444540	AI693927	Hs.265165 ESTs	4.0
20	415579	AA165232	Hs.222059 ESTs	4.0
	452891	N75582	Hs.212875 ESTs, Weakly similar to DYH9_HUMAN CILIA	4.0
	414605	BE390440	gb:601283601F1 NIH_MGC_44 Homo sapiens c	4.0
	452281	T93500	Hs.28792 Homo sapiens cDNA FLJ11041 fls, clone PL	4.0
	417801	AA417383	Hs.82582 integrin, beta-like 1 (with EGF-like rep	4.0
25	446232	AI281848	Hs.194691 retinoic acid induced 3	4.0
	447377	X77343	Hs.334334 transcription factor AP-2 alpha (activat	4.0
	437854	AL119723	gb:DKFZp761A2124_r1 761 (synonym: hamy2)	4.0
	446140	AA356170	Hs.26750 hypothetical protein FLJ21908	4.0
	452240	AI591147	Hs.61232 ESTs	4.0
30	459574	AI741122	Hs.101810 Homo sapiens cDNA FLJ14232 fls, clone NT	4.0
	458673	N99626	gb:za39d11.r1 Soares fetal liver spleen	4.0
	444858	AI199738	Hs.208275 ESTs, Weakly similar to ALUA_HUMAN !!!!	4.0
	452166	AI948607	Hs.264680 ESTs	4.0
35	452681	AF153330	Hs.30246 solute carrier family 19 (thiamine trans	3.9
	450192	AA263143	Hs.24596 RAD51-interacting protein	3.9
	406554	NA	Target Exon	3.9
	416259	AA573006	Hs.19173 ESTs	3.9
	445813	Z42023	Hs.106576 alanine-glyoxylate aminotransferase 2-II	3.9
	451024	AA442176	gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_	3.9
40	413930	M86153	Hs.75618 RAB11A, member RAS oncogene family	3.9
	401781		Target Exon	3.9
	415296	F05086	Hs.328142 ESTs	3.9
	452564	AA026777	gb:ze93c11.r1 Soares_fetal_heart_NbHH19W	3.9
	442500	AI819068	Hs.209122 ESTs	3.9
45	419759	Z21336	Hs.135411 actin related protein	3.9
	424638	AI472106	Hs.49303 Homo sapiens cDNA FLJ11663 fls, clone HE	3.9
	439699	AF086534	Hs.187561 ESTs, Moderately similar to ALU1_HUMAN A	3.9
	428042	AA419529	Hs.76391 myxovirus (influenza) resistance 1, homo	3.9
	452501	AB037791	Hs.29716 hypothetical protein FLJ10980	3.9
50	453049	BE537217	Hs.30343 ESTs	3.9
	443213	BE568414	Hs.145497 Homo sapiens cDNA: FLJ22097 fls, clone H	3.9
	443469	AI073512	Hs.133916 ESTs	3.9
	455092	BE152428	gb:CM0-HT0323-151299-126-b04 HT0323 Homo	3.9
	401785		NM_002275*:Homo sapiens keratin 15 (KRT1	3.9
55	426427	M86699	Hs.169840 TTK protein kinase	3.9
	446009	AI989885	Hs.231926 ESTs	3.9
	436033	H75391	Hs.255748 ESTs	3.9
	451067	BE172186	gb:MR0-HT0559-110300-005-h11 HT0559 Homo	3.8
	419348	AA236845	Hs.98274 ESTs	3.8
60	444635	AI184268	Hs.339665 ESTs	3.8
	412140	AA219691	Hs.73625 RAB6 interacting, kinesin-like (rabkines	3.8
	403593	NA	Target Exon	3.8
	442323	AW016669	Hs.29190 ESTs	3.8
	419854	AW664873	Hs.87836 Homo sapiens PAC clone RP5-1087M19 from	3.8
65	433871	W02410	Hs.205555 ESTs	3.8
	445253	AI217928	Hs.144762 ESTs	3.8
	409542	AA503020	Hs.36563 hypothetical protein FLJ22418	3.8

	443162	T49951	Hs.9029	DKFZP434G032 protein	3.8
	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	3.8
	422475	AL359938	Hs.117313	Mals (mouse) homolog 3	3.8
	440705	AA904244	Hs.153205	ESTs	3.8
5	447290	AI476732	Hs.263912	ESTs	3.8
	403426			Target Exon	3.8
	427821	AA470158	Hs.98202	ESTs	3.8
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b p.H.sap	3.8
	443801	AW206942	Hs.253594	ESTs	3.8
10	410658	AW105231	Hs.192035	ESTs	3.8
	410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo3.8	
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.8
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypothe	3.8
	447935	AI742618	Hs.181733	ESTs, Weakly similar to nitrilase homolo	3.7
15	401747			Homo sapiens keratin 17 (KRT17)	3.7
	420633	NM_014581	Hs.274480	odorant-binding protein 2A	3.7
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.7
	433138	AB029496	Hs.59729	semaphorin sem2	3.7
	434715	BE005346	Hs.116410	ESTs	3.7
20	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.7
	450951	AA018534	Hs.103334	ESTs	3.7
	402696	NA		C3002523:gl 686211 sp Q27533 YH2M_CAEEL3.7	
	446868	AV660737	Hs.135100	ESTs	3.7
25	458154	AW816379	Hs.335018	ESTs	3.7
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	3.7
	419440	AB020689	Hs.90419	KIAA0882 protein	3.7
	421524	AA312062	Hs.105445	GDNF family receptor alpha 1	3.7
	417283	N62840	Hs.48648	ESTs	3.7
	401508	NA		NM_024817:Homo sapiens hypothetical prot	3.7
30	410303	AA324597	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	3.7
	420362	U79734	Hs.97206	huntingtin interacting protein 1	3.7
	433384	AI021992	Hs.124244	ESTs	3.7
	434302	AA629065	Hs.116301	ESTs	3.7
	443938	R55373	Hs.20864	ESTs	3.7
35	448420	BE623004		gb:601441282F1 NIH_MGC_72 Homo sapiens c	3.7
	458712	AI347502	Hs.107872	hypothetical protein FLJ20761	3.7
	433404	T32982	Hs.102720	ESTs	3.7
	405232			NM_015832:Homo sapiens methyl-CpG bindin	3.7
40	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.7
	455609	BE011668		gb:CM3-BN0223-100500-177-a04 BN0223 Homo3.7	
	450164	AI239923	Hs.30098	ESTs	3.7
	453948	AI970797	Hs.64859	ESTs	3.7
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	3.7
	401049	NA		Target Exon	3.6
45	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	3.6
	420179	N74530	Hs.21168	ESTs	3.6
	458663	AV658444	Hs.260776	tankyrase, TRF1-interacting ankyrin-rela	3.6
	437259	AI377755	Hs.120695	ESTs	3.6
50	428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	3.6
	450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.6
	451952	AL120173	Hs.301663	ESTs	3.6
	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo3.6	
	425201	AA352111		gb:EST60061 Activated T-cells XX Homo sa	3.6
	443830	AI142095	Hs.143273	ESTs	3.6
55	439255	BE164500		gb:RC4-HT0469-230300-014-e10 HT0469 Homo3.6	
	414869	AA157291	Hs.21479	ubiquitin 1	3.6
	409064	AA062954	Hs.141883	ESTs	3.6
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	3.6
	445135	AK000054	Hs.12347	hypothetical protein FLJ20047	3.6
60	404091	NA		Target Exon	3.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	3.6
	405153			Target Exon	3.6
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	3.6
	403639	NA		ENSPD0000233023*:CDNA FLJ12652 fis, clon	3.6
65	404360			C7001385:gl 12082809 gb AAG48618.1 AF315	3.6
	422352	AA766296	Hs.99200	ESTs	3.6
	423338	AB007961	Hs.127338	KIAA0492 protein	3.6

	424202	BE350295	Hs.15032	RAN binding protein 17	3.6
	431750	AA514986	Hs.283705	ESTs	3.6
	439937	AA853978	Hs.124577	ESTs	3.6
5	453596	AA441838	Hs.62905	hypothetical protein FLJ14834	3.6
	406446	NA		Target Exon	3.6
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.6
	434360	AW015415	Hs.127780	ESTs	3.6
	409079	W87707	Hs.82085	interleukin 6 signal transducer (gp130,	3.6
10	440132	AI697121	Hs.202466	ESTs, Weakly similar to S65824 reverse t	3.6
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	3.6
	440671	AW297920	Hs.130954	ESTs	3.5
	407647	AW860158		gb:RC0-CT0379-290100-032-b04 CT0379 Homo	3.5
	459023	AW968226	Hs.60798	ESTs	3.5
	402820			NM_017646*:Homo sapiens tRNA isopentenyl	3.5
15	417009	AA191719	Hs.314714	ESTs	3.5
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	3.5
	449978	AI806335	Hs.200829	ESTs, Weakly similar to T30171 nina1 -	3.5
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	3.5
	452909	NM_015358	Hs.30985	pannexin 1	3.5
20	400610	NA		Target Exon	3.5
	417843	W07361	Hs.22545	Homo sapiens cDNA FLJ12935 fls, clone NT	3.5
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	3.5
	451592	AI806416	Hs.213897	ESTs	3.5
	443270	NM_004272	Hs.337737	Homer, neuronal immediate early gene, 1B	3.5
25	423848	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	3.5
	449424	AW448937	Hs.197030	ESTs	3.5
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.5
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	3.5
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.5
30	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	3.5
	415778	H84847	Hs.49391	hypothetical protein LOC54149	3.5
	413054	AW316843	Hs.66309	hypothetical protein MGC11061	3.5
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	3.5
	424639	AI917494	Hs.9812	Homo sapiens cDNA FLJ14388 fls, clone HE	3.5
35	424627	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fls, clone L	3.5
	437782	AI370876	Hs.79090	exportin 1 (CRM1, yeast, homolog)	3.5
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	3.5
	413783	AA314337	Hs.301547	ribosomal protein S7	3.5
	421105	AA877124	Hs.172844	ESTs	3.5
40	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	3.5
	440623	AI935016	Hs.216639	ESTs	3.5
	455838	BE145808		gb:MRO-HT0208-101299-103-f11 HT0208 Homo	3.5
	458771	AW295151	Hs.163612	ESTs	3.5
	442942	AW167087	Hs.131562	ESTs	3.5
45	436550	Z50158	Hs.270235	ESTs, Weakly similar to MMHUB1 laminin b	3.5
	418849	AW474547	Hs.53585	Homo sapiens PIG-M mRNA for mannosyltran	3.5
	424420	BE614743	Hs.146688	prostaglandin E synthase	3.5
	430916	AW505021	Hs.88414	BTB and CNC homology 1, basic leucine zi	3.5
	432030	AI908400	Hs.143789	ESTs	3.5
50	439405	AF086224	Hs.55238	ESTs	3.5
	405917	NA		C17000675:gi7290703 gb AAF46150.1 (AEO	3.5
	452727	AW993582	Hs.176220	ESTs	3.5
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.4
	421070	AA283185	Hs.19327	ESTs	3.4
55	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila inaD-like	3.4
	428508	BE252383	Hs.184658	SBBI31 protein	3.4
	455651	BE064962		gb:RC1-BT0313-130400-016-c02 BT0313 Homo	3.4
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.4
	447754	AW073310	Hs.163533	Homo sapiens cDNA FLJ14142 fls, clone MA	3.4
60	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	3.4
	404097	NA		C5000242*:gi9369379 gb AAF87128.1 AC006	3.4
	434205	AF119861	Hs.283032	hypothetical protein PRO2015	3.4
	421072	AI215069	Hs.89113	ESTs	3.4
	402421	NA		C1001578*:gi759903 gb AAF28099.1 (AF1	3.4
65	405248	NA		Target Exon	3.4
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	3.4
	403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	3.4

	433393	AF038564	Hs.98074	Itchy (mouse homolog) E3 ubiquitin prote	3.4
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	3.4
	458747	BE318395	Hs.257391	hypothetical protein DKFZp761J1523	3.4
	442082	R41823	Hs.7413	ESTs; calyntenin-2	3.4
5	417974	AA210765		gb:zr90c06.r1 NCL_CGAP_GCB1 Homo sapiens	3.4
	446002	AI346468	Hs.145789	ESTs	3.4
	448995	AI613276	Hs.5682	guanine nucleotide binding protein (G pr	3.4
	436007	AI247716	Hs.232168	ESTs	3.4
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	3.4
10	435202	AI971313	Hs.170204	KIAA0551 protein	3.4
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.3
	405460	NA		Target Exon	3.3
	441826	AW503603	Hs.129915	phospholipase related	3.3
	453472	AL037925		gb:DKFZp564M037_r1 564 (synonym: hibr2)	3.3
15	447078	AW885727	Hs.301570	ESTs	3.3
	441690	R81733	Hs.33106	ESTs	3.3
	420092	AA814043	Hs.88045	ESTs	3.3
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.3
	408908	BE295227	Hs.250822	serine/threonine kinase 15	3.3
20	414737	AI160386	Hs.125087	ESTs	3.3
	449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	3.3
	418912	NM_000685	Hs.89472	angiotensin receptor 1	3.3
	438405	AA160079	Hs.172932	Homo sapiens mRNA for partial 3'UTR, seq	3.3
	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	3.3
25	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	3.3
	429548	AW138872	Hs.135288	ESTs	3.3
	420807	AA280627	Hs.57846	ESTs	3.3
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sa	3.3
	445189	AI936450	Hs.147482	ESTs	3.3
30	402892	NA		Target Exon	3.3
	426681	AA994896	Hs.22514	ESTs	3.3
	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypothe	3.3
	409430	R21945	Hs.166975	splicing factor, arginine/serine-rich 5	3.3
	443194	AI954968	Hs.279009	matrix Gla protein	3.3
35	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.3
	410908	AA121686	Hs.10592	ESTs	3.3
	405151	NA		Target Exon	3.3
	436461	AW511956	Hs.293261	ESTs	3.3
40	411171	AW820260		gb:QV2-ST0296-150200-040-c10 ST0296 Homo	3.3
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.3
	439310	AF086120	Hs.102793	ESTs	3.3
	401575	NA		Target Exon	3.3
	420900	AL045633	Hs.44269	ESTs	3.3
	445628	AI344166	Hs.155743	ESTs	3.3
45	448243	AW369771	Hs.52620	integrin, beta 8	3.3
	445102	AW204610	Hs.22270	ESTs	3.3
	442118	AA976718	Hs.202242	ESTs	3.3
	416783	AA206186	Hs.79889	monocyte to macrophage differentiation-a	3.3
50	435039	AW043921	Hs.130526	ESTs	3.3
	451474	T70874	Hs.207636	ESTs	3.2
	442559	T10213	Hs.159993	glycosyltransferase	3.2
	453921	AI824009	Hs.44577	ESTs	3.2
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp5861823 (f	3.2
	435627	W88774	Hs.118370	ESTs	3.2
55	411596	BE336654	Hs.70937	H3 histone family, member A	3.2
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	3.2
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	3.2
	403637	NA		C3001106*gi10047201 dbj BAB13394.1 (A	3.2
	405547			NM_018833*-Homo sapiens transporter 2, A	3.2
60	427878	C05766	Hs.181022	CGI-07 protein	3.2
	451871	AI821005	Hs.118599	ESTs	3.2
	410313	R10305	Hs.185683	ESTs	3.2
	416856	N27833	Hs.269028	ESTs, Weakly similar to I38022 hypothe	3.2
	449490	AI652777	Hs.197069	ESTs	3.2
65	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	3.2
	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H	3.2
	459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypothe	3.2

	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	3.2
	430965	AA489732	Hs.154918	ESTs	3.2
	405394			Target Exon	3.2
5	424693	BE169810	Hs.47557	ESTs	3.2
	454265	H03556	Hs.300949	ESTs, Weakly similar to thyroid hormone	3.2
	437687	AA765917	Hs.122840	ESTs	3.2
	428372	AK000684	Hs.183887	hypothetical protein FLJ22104	3.2
	414083	AL121282	Hs.257786	ESTs	3.2
10	411670	AW856552		gb:RC1-CT0294-080100-012-a04 CT0294 Homo	3.2
	416283	NM_035429	Hs.79141	vascular endothelial growth factor C	3.2
	437488	AA758239	Hs.180330	ESTs	3.2
	428398	AI249368	Hs.98558	ESTs	3.2
	452042	H38857	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	3.2
15	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	3.2
	438078	AI016377	Hs.131693	ESTs	3.2
	448816	AB033052	Hs.22151	KIAA1226 protein	3.2
	419519	AI198719	Hs.176376	ESTs	3.2
	404580			NM_014112*:Homo sapiens trichorhinophala	3.2
20	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.2
	457473	AW974903	Hs.291231	ESTs	3.1
	429838	AW904907	Hs.30732	hypothetical protein FLJ13409; KIAA1711	3.1
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	3.1
	400195	NA		NM_007057*:Homo sapiens ZW10 Interactor	3.1
25	417860	AW408557	Hs.235498	hypothetical protein FLJ14075	3.1
	417995	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICRO	3.1
	422589	AA312735	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	3.1
	435870	AA701327	Hs.17949	ESTs	3.1
	440801	AA906366	Hs.190535	ESTs	3.1
30	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily	3.1
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	3.1
	439677	R82331	Hs.164599	ESTs	3.1
	452834	AI638627	Hs.105685	KIAA1688 protein	3.1
35	431349	AA503653	Hs.156942	ESTs, Moderately similar to ALU2_HUMAN A	3.1
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	3.1
	430284	AA470519		gb:nc71f10.s1 NCL_CGAP_Pr1 Homo sapiens	3.1
	418827	BE327311	Hs.47166	HT021	3.1
	410835	AW806906		gb:QV4-ST0023-160400-172-d12 ST0023 Homo	3.1
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.1
40	405336	NA		Target Exon	3.1
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	440931	AI583052	Hs.270058	ESTs	3.1
	455945	BE160636		gb:PM1-HT0422-291299-002-c08 HT0422 Homo	3.1
	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.1
45	405848	NA		Target Exon	3.1
	455685	BE069976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	3.1
	406970	M29994		gb:Human alpha-I spectrin gene, exon 12.	3.1
	409602	W26713	Hs.256972	ESTs	3.1
	423518	D45027	Hs.129732	R3H domain (binds single-stranded nucle	3.1
50	425653	AI065104	Hs.249718	ESTs, Weakly similar to A46010 X-linked	3.1
	426326	BE165753	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.1
	433805	AA706910	Hs.112742	ESTs	3.1
	437152	AL050027		gb:Homo sapiens mRNA; cDNA DKFZp566C03243.1	3.1
	448602	AI541305	Hs.48778	niban protein	3.1
55	452844	AW407181	Hs.218377	Homo sapiens cDNA FLJ11927 fis, clone HE	3.1
	407366	AF026942		gb:Homo sapiens c1g33 mRNA, partial sequ	3.1
	408254	AW807227		gb:MR4-ST0062-180200-001-e10 ST0062 Homo	3.1
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.1
	416790	R83066	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	3.1
60	420020	BE295686	Hs.94382	adenosine kinase	3.1
	426119	W94997	Hs.189917	ESTs	3.1
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	3.1
	457421	AL117431	Hs.112165	Homo sapiens cDNA FLJ12198 fis, clone MA	3.1
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	3.1
	454141	AW138413	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
65	426650	AA382814		gb:EST96097 Testis 1 Homo sapiens cDNA 5	3.1
	450865	AI246013	Hs.105532	ESTs, Weakly similar to i38588 reverse t	3.1
	407993	AW135274	Hs.12433	ESTs	3.1

	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	3.1
	457888	BE219794	Hs.293471	ESTs	3.1
	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	3.0
	409248	AB033035	Hs.51965	KIAA1209 protein	3.0
5	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.0
	418926	AA232658	Hs.105794	UDP-glucose:glycoprotein glucosyltransfe	3.0
	419346	AI830417	Hs.44143	polybromo 1	3.0
	429826	N93266	Hs.40747	ESTs	3.0
	435447	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f3.0	3.0
10	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	3.0
	405609	NA		ENSP00000241065*.CDNA	3.0
	404274			NM_002944*.Homo sapiens v-ros avian UR2	3.0
	448777	AI971362	Hs.231945	ESTs	3.0
	415459	H07118	Hs.6099	ESTs	3.0
15	415245	N59650	Hs.27252	ESTs	3.0
	406291	NA		Target Exon	3.0
	414210	BE383592		gb:601297871F1 NIH_MGC_19 Homo sapiens c	3.0
	432055	AW972359	Hs.293334	ESTs	3.0
	442246	AI791988	Hs.129115	ESTs	3.0
20	451353	N21043	Hs.42932	ESTs	3.0
	451177	AI969716	Hs.13034	ESTs	3.0
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	3.0
	401326	NA		C10000447*.gil1168375[sp]P43457[AGA1_PED	3.0
	408920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	3.0
25	432887	AI926047	Hs.162859	ESTs	3.0
	411789	AF245505	Hs.72157	DKFZP5641922 protein	3.0
	401045			C11001883*.gil6753278[ref]NP_033938.1 c	3.0
	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	3.0
	434627	AI221894	Hs.39311	ESTs	3.0
30	442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	3.0
	425477	AW958879	Hs.270535	ESTs	3.0
	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.0
	433014	NM_014711	Hs.279912	KIAA0419 gene product	3.0
	415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypotheti	3.0
35	416173	R52782		gb:yg99d09.r1 Soares infant brain 1N1B H	3.0
	406155	AB014528	Hs.43133	KIAA0628 gene product	3.0
	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.0
	435485	AI754212	Hs.21951	Homo sapiens Xq pseudoautosomal region;	3.0
	423529	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.0
40	411836	AW901879	Hs.314453	ESTs	3.0
	415030	D31118	Hs.191735	hypothetical protein MGC10520	3.0
	419606	AW294795	Hs.198529	ESTs	3.0
	440310	AA876939	Hs.125406	ESTs	3.0
	443608	AI375957	Hs.289074	F-box only protein 22	3.0
45	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	3.0
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	3.0
	435393	AA701259	Hs.189299	ESTs	3.0
	454071	AI041793	Hs.42502	ESTs	3.0
	446922	BE175605		gb:RC5-HT0580-100500-022-H07 HT0580 Homo	3.0
50	448062	AW295923	Hs.255472	KIAA1843 protein	3.0
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	3.0
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	3.0
	424866	W01938	Hs.337243	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	2.9
55	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.9
	445625	BE246743	Hs.288529	hypothetical protein FLJ22635	2.9
	403677	NA		C4001462:gil4887715[gb]AAA79329.2 (L088	2.9
	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	2.9
	435255	W87434	Hs.106015	ESTs, Moderately similar to ALU1_HUMAN A	2.9
60	443127	BE568102	Hs.180312	mitochondrial ribosomal protein S16	2.9
	449104	AI674818	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HE	2.9
	427315	AA179949	Hs.175583	Homo sapiens mRNA; cDNA DKFZp564N0763 (f2.9	2.9
	430414	AW365665	Hs.120388	ESTs	2.9
	423600	AI633559	Hs.310359	ESTs	2.9
65	458562	N34128	Hs.145268	ESTs	2.9
	402109	NA		Target Exon	2.9
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	2.9

	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	2.9
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
	404721			NM_005596*:Homo sapiens nuclear factor I	2.9
5	445107	AI208121	Hs.147313	ESTs, Weakly similar to I38022 hypothe	2.9
	401987			NM_002737*:Homo sapiens protein kinase C	2.9
	430566	AA481282	Hs.190149	ESTs	2.9
	444517	AI939339	Hs.146883	ESTs	2.9
	445563	AW873606	Hs.149006	ESTs	2.9
10	427691	AW194426	Hs.20726	ESTs	2.9
	456561	AI868634	Hs.246358	ESTs, Weakly similar to T32250 hypothe	2.9
	401458			Target Exon	2.9
	421039	NM_003478	Hs.101299	culin 5	2.9
	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	2.9
15	424862	NM_012288	Hs.153954	TRAM-like protein	2.9
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 f	2.9
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	2.9
	413221	BE161151		gb:PMO-HT0425-141299-001-F08 HT0425 Homo	2.9
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	2.9
20	433687	AA743991		gb:ny57g01.s1 NCI_CGAP_Pr18 Homo sapiens	2.9
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypothe	2.9
	454529	Z45439	Hs.270425	ESTs	2.9
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.9
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	2.9
25	457402	AW452648	Hs.149342	activation-induced cytidine deaminase	2.9
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.9
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	2.9
	401093			C12000586*:gi 6330167 dbj BAA86477.1 (A	2.9
	435061	AI651474	Hs.163944	ESTs	2.9
30	447985	AI681475	Hs.200949	ESTs	2.9
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	2.9
	426384	AI472078	Hs.303662	ESTs	2.9
	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	2.9
	405953	NA		Target Exon	2.8
35	420854	AW296927		gb:U1-H-BW0-ajc-c-07-0-U1.s1 NCI_CGAP_Su	2.8
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	2.8
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	2.8
	442861	AA243837	Hs.57787	ESTs	2.8
	448337	AW206453	Hs.3782	ESTs	2.8
40	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.8
	412248	BE176480		gb:RC3-HT0585-160300-022-c02 HT0585 Homo	2.8
	449450	AL039852	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	2.8
	434757	AI038997	Hs.132921	ESTs	2.8
	408038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.8
45	454545	AW806899		gb:QV4-ST0023-160400-172-c12 ST0023 Homo	2.8
	439842	AI910895	Hs.132413	ESTs	2.8
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.8
	424800	AL035588	Hs.153203	MyoD family inhibitor	2.8
	411086	BE070800		gb:RC3-BT0502-251199-011-c07 BT0502 Homo	2.8
	400250	NA		Eos Control	2.8
50	449168	NM_016206	Hs.23142	colon carcinoma related protein	2.8
	456482	AA485224		gb:aa41b12.s1 NCI_CGAP_GCB1 Homo sapiens	2.8
	426044	AA502490	Hs.336895	ESTs	2.8
	431854	AA383550	Hs.271699	polymerase (DNA directed) Iota	2.8
	405873	NA		Target Exon	2.8
55	440400	AA994394	Hs.125594	ESTs, Weakly similar to T25472 hypothe	2.8
	458265	AI075375	Hs.128193	ESTs, Weakly similar to IRIX2_HUMAN IROQU	2.8
	413708	BE158791		gb:IL2-HT0397-091299-025-D02 HT0397 Homo	2.8
	423739	AA396155	Hs.97600	ESTs	2.8
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.8
60	453096	AW294631	Hs.11325	ESTs	2.8
	421825	AA296758	Hs.183747	ESTs, Moderately similar to CALB_HUMAN C	2.8
	417742	R54719		gb:EST22d11 WATM1 Homo sapiens cDNA clon	2.8
	402765			C1003621*:gi 12407405 gb AAG53491.1 AF22	2.8
	444378	R41339	Hs.12569	ESTs	2.8
65	419172	AW338625	Hs.22120	ESTs	2.8
	401497			Target Exon	2.8
	402376			C19000763*:gi 1363912 pir JC4296 ring f	2.8

	405041	NA	C3001706*:g 1345652 sp P15989 CA36_CHIC	2.8
	408758	NM_003686	Hs.47504 exonuclease 1	2.8
	431917	D16181	Hs.2868 peripheral myelin protein 2	2.8
	437583	AA761190	Hs.244627 ESTs	2.8
5	453737	AA744862	Hs.194293 ESTs, Weakly similar to I54374 gene NF2	2.8
	458094	AF086325	gb:Homo sapiens full length insert cDNA	2.8
	401283	NA	Target Exon	2.8
	410784	AW803201	gb:IL2-UM0077-070500-080-E06 UM0077 Homo	2.8
	417601	NM_014735	Hs.82292 KIAA0215 gene product	2.8
10	418236	AW994005	Hs.337534 ESTs	2.8
	435532	AW291488	Hs.117305 Homo sapiens, clone IMAGE:3682908, mRNA	2.8
	454714	AW815098	gb:QV4-ST0212-091:99-023-f10 ST0212 Homo	2.8
	418629	BE247550	Hs.86859 growth factor receptor-bound protein 7	2.8
	442101	AI651930	Hs.135684 ESTs	2.8
15	405080	AK000375	Hs.88820 HDCMC28P protein	2.8
	414661	T97401	Hs.21929 ESTs	2.8
	425589	AI850633	Hs.143688 Homo sapiens cDNA: FLJ23031 fis, clone L	2.8
	429638	AI918662	Hs.211577 kinesin 1 (kinesin receptor)	2.7
	428824	W23624	Hs.173059 ESTs	2.7
20	421566	NM_000399	Hs.1395 early growth response 2 (Krox-20 (Drosop	2.7
	414596	BE386870	gb:601275271F1 NIH_MGC_20 Homo sapiens c	2.7
	440868	R79707	Hs.263339 ESTs, Moderately similar to I38022 hypot	2.7
	452943	BE247449	Hs.31082 hypothetical protein FLJ10525	2.7
	443772	AV846449	Hs.282872 ESTs	2.7
25	432361	AI378562	Hs.159585 ESTs	2.7
	430375	AW371048	Hs.93758 H4 histone family, member H	2.7
	406504	NA	C5000558:g 4504675 ref NP_002175.1 int	2.7
	423279	AW959861	Hs.290943 ESTs	2.7
	424871	NM_004525	Hs.153595 low density lipoprotein-related protein	2.7
30	453619	H87648	Hs.33922 Homo sapiens, clone MGC:9084, mRNA, comp	2.7
	423961	D13666	Hs.136348 osteoblast specific factor 2 (fasciclin	2.7
	422156	N34524	gb:yy56d10.s1 Soares_multiple_sclerosis_	2.7
	415752	BE314524	Hs.78776 putative transmembrane protein	2.7
	419987	NM_005014	Hs.94070 osteomodulin	2.7
35	406182	NA	Target Exon	2.7
	416495	X69970	Hs.79350 RYK receptor-like tyrosine kinase	2.7
	444701	AI916512	Hs.198394 ESTs	2.7
	408171	AA301228	Hs.43299 hypothetical protein FLJ12890	2.7
	430153	AW968128	Hs.336679 ESTs	2.7
40	413383	AA128978	Hs.154706 hypothetical protein FLJ14917	2.7
	414831	M31158	Hs.77439 protein kinase, cAMP-dependent, regulato	2.7
	413278	BE563085	Hs.833 interferon-stimulated protein, 15 kDa	2.7
	433132	AB026264	Hs.284245 hypothetical protein IMPACT	2.7
	437030	AA742577	Hs.303781 EST	2.7
45	439031	AF075079	gb:Homo sapiens full length insert cDNA	2.7
	449532	W74853	Hs.271593 ESTs, Moderately similar to A47582 B-cel	2.7
	406153		Target Exon	2.7
	406625	Y13647	Hs.119597 stearyl-CoA desaturase (delta-9-desatur	2.7
50	444698	AI188139	Hs.147050 ESTs	2.7
	432328	AI572739	Hs.195471 6-phosphofructo-2-kinase/fructose-2,6-bi	2.7
	429628	H09604	Hs.13268 ESTs	2.7
	420149	AA255920	Hs.88095 ESTs	2.7
	431207	AA495925	Hs.9394 ESTs	2.7
	438394	BE379623	Hs.27693 peptidylprolyl isomerase (cyclophilin)-I	2.7
55	443304	AI050073	Hs.135338 ESTs	2.7
	427660	AI741320	Hs.114121 Homo sapiens cDNA: FLJ23228 fis, clone C	2.7
	408460	AA054726	Hs.285574 ESTs	2.7
	416515	N91716	Hs.194140 ESTs, Weakly similar to I38022 hypothet	2.7
	429922	Z97630	Hs.226117 H1 histone family, member O	2.7
60	418203	X54942	Hs.83758 CDC28 protein kinase 2	2.7
	439509	AF086332	Hs.58314 ESTs	2.7
	402184	NA	ENSP00000245238*:cDNA FLJ10922 fis, clon	2.7
	450496	AW449251	Hs.257131 ESTs	2.7
	451963	AI825440	Hs.224962 ESTs	2.7
65	457938	AI373638	Hs.133900 ESTs	2.7
	441541	AA938663	Hs.199828 ESTs	2.7
	441111	AI806867	Hs.126594 ESTs	2.7

	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
	445354	AV653485	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA,	2.7
	427961	AW293165	Hs.143134	ESTs	2.7
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	2.7
5	445234	AW137636	Hs.146059	ESTs	2.7
	413903	AA496493	Hs.23136	ESTs	2.7
	406069	NA		Target Exon	2.7
	447410	AI470235	Hs.172698	EST	2.7
	401256	NA		NM_024089*:Homo sapiens hypothetical pro	2.7
10	415139	AW975942	Hs.48524	ESTs	2.7
	420218	AW958037	Hs.286	ribosomal protein L4	2.7
	455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	2.7
	438825	BE327427	Hs.79953	ESTs	2.6
	409584	AA045857	Hs.54943	fracture callus 1 (rat) homolog	2.6
15	452837	AL121053	Hs.5534	Homo sapiens cDNA FLJ12961 fls, clone NT	2.6
	434876	AF160477	Hs.61460	lg superfamily receptor LNIR	2.6
	421565	AK001122	Hs.105859	hypothetical protein FLJ10250	2.6
	453279	AW893940	Hs.59698	ESTs	2.6
	430785	Z30201		gb:HHEA22G Atrium cDNA library Human hea	2.6
20	455986	D38299	Hs.170917	prostaglandin E receptor 3 (subtype EP3)	2.6
	433068	NM_006456	Hs.288215	sialyltransferase	2.6
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	2.6
	429208	AA447990	Hs.190478	ESTs	2.6
	430733	AW975920	Hs.283361	ESTs	2.6
25	441720	AI346487	Hs.28739	ESTs	2.6
	418986	AI123555	Hs.81796	ESTs	2.6
	432481	AW451645	Hs.151504	Homo sapiens cDNA FLJ11973 fls, clone HE	2.6
	434338	AW754311		gb:CM1-CT0337-141299-068-f07 CT0337 Homo	2.6
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fls, clone HE	2.6
30	410530	M25809	Hs.64173	ATPase, H transporting, lysosomal (vacuo	2.6
	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	2.6
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.6
	408868	AW292286	Hs.255058	ESTs	2.6
	451531	AA018311	Hs.114762	ESTs	2.6
35	405822			Target Exon	2.6
	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.6
	417315	AI080042	Hs.336901	ribosomal protein S24	2.6
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fls, clone HE	2.6
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fls, clone NT	2.6
40	405638			Target Exon	2.6
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	2.6
	403943			C5000355:gil4503225[re]NP_000765.1] cyt	2.6
	404535	Z25884	Hs.121483	chloride channel 1, skeletal muscle (Th	2.6
	402800	NA		Target Exon	2.6
45	449144	AI989503	Hs.233405	ESTs	2.6
	454934	AW846080	Hs.314324	ESTs	2.6
	424717	H03754	Hs.152213	wingless-type MMTV Integration site fami	2.6
	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	2.6
	427970	AA418187	Hs.330515	ESTs	2.6
50	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	2.6
	453034	BE246010	Hs.271468	Homo sapiens mRNA for FLJ00038 protein,	2.6
	455097	AW855802		gb:RC1-CT0279-170200-023-d08 CT0279 Homo	2.6
	427317	AB028955	Hs.175780	KIAA1032 protein	2.6
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.6
55	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	2.6
	423201	NM_000163	Hs.125180	growth hormone receptor	2.6
	406271			Target Exon	2.6
	442696	BE566962	Hs.7063	Homo sapiens cDNA: FLJ20913 fls, clone A	2.6
	454018	AW016892	Hs.100855	ESTs	2.6
60	435420	AI928513	Hs.59203	ESTs	2.6
	434398	AA121098	Hs.3838	serum-inducible kinase	2.6
	455708	BE069326		gb:QV3-BT0361-170100-060-g03 BT0361 Homo	2.6
	438347	W24320	Hs.102941	Homo sapiens cDNA: FLJ21531 fls, clone C	2.6
	407523	X64984		gb:H.sapiens mRNA HTPCRX10 for olfactory	2.6
65	425101	AA830431	Hs.180811	ESTs	2.6
	435153	AA668763	Hs.291939	ESTs	2.6
	409139	AI681917	Hs.3321	ESTs, Highly similar to IRIX1_HUMAN IROQU	2.6

	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	2.6
	414612	BE274562	Hs.76578	protein inhibitor of activated STAT3	2.6
	440283	AI732892	Hs.190489	ESTs	2.6
5	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.6
	431473	AA825686	Hs.321176	ESTs, Weakly similar to S65824 reverse t	2.6
	404440			NM_021048:Homo sapiens melanoma antigen,	2.6
	403388	NA		C3001398*gi12248917 dbj BAB20375.1 (A	2.6
	403775	NA		Target Exon	2.6
	405037	NA		NM_021628*:Homo sapiens arachidonate lip	2.6
10	407447	AF290544		gb:Homo sapiens aminopeptidase mRNA, par	2.6
	420952	AA282067	Hs.88972	ESTs, Moderately similar to A46010 X-in	2.6
	435447	AI872932		gb:wm72e03.x1 NCI_CGAP_U12 Homo sapiens	2.6
	440202	AW516211	Hs.125300	ring finger protein 21, interferon-respo	2.6
	445854	AI702885	Hs.145568	ESTs	2.6
15	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.6
	414870	N72264	Hs.300670	KIAA1204 protein	2.6
	457411	AW085961	Hs.130093	ESTs	2.6
	424676	Y08565	Hs.151678	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.6
	404443			C8001428*gi16572242 emb CAB62951.1 (Z9	2.6
20	452268	NM_003512	Hs.28777	H2A histone family, member L	2.6
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	2.6
	444779	AI192105	Hs.147170	ESTs	2.6
	408633	AW963372	Hs.46677	PRO2000 protein	2.6
	469089	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f2	2.6
25	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.6
	454111	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypothel	2.6
	411465	NM_000169	Hs.69089	galactosidase, alpha	2.6
	406922	S70284		gb:stearoyl-CoA desaturase (human, adipo	2.6
	456045	H62943	Hs.154188	ESTs	2.6
30	413111	BE065837		gb:RC2-BT0318-110100-012-g12 BT0318 Homo	2.6
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selen	2.6
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	2.5
	427032	AF012023	Hs.173274	integrin cytoplasmic domain-associated p	2.5
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	2.5
35	422225	BE245652	Hs.118281	zinc finger protein 266	2.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (MMP7; uterin	2.5
	410011	AB020641	Hs.57856	PFTAIKE protein kinase 1	2.5
	426310	NM_000909	Hs.169266	neuropeptide Y receptor Y1	2.5
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	2.5
40	437770	AA767881	Hs.122897	ESTs	2.5
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	2.5
	414251	AL042308	Hs.97689	VASA protein	2.5
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothel	2.5
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	2.5
45	455732	BE080908		gb:QV1-BT0631-280200-064-h07 BT0631 Homo	2.5
	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.5
	428257	BE394723	Hs.275243	S100 calcium-binding protein A6 (calcycl	2.5
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.5
	458652	AW375610	Hs.117102	hypothetical protein FLJ13046 similar to	2.5
50	458012	AI424999	Hs.188211	ESTs	2.5
	422996	BE091089		gb:PM4-BT0724-130400-006-c07 BT0724 Homo	2.5
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	2.5
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	2.5
	440029	AW089705	Hs.293711	ESTs, Weakly similar to S64329 probable	2.5
55	448141	AI471598	Hs.197531	ESTs	2.5
	409163	AA065081		gb:zm13a03.s1 Stratagene pancreas (93720	2.5
	431386	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	2.5
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	2.5
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.5
60	455935	BE158687		gb:CM0-HT0395-280100-169-b09 HT0395 Homo	2.5
	425025	AW953168	Hs.12407	ESTs	2.5
	416589	AA652687	Hs.95151	Human DNA sequence from clone RP5-1103G7	2.5
	404826			Target Exon	2.5
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	2.5
65	421991	NM_014918	Hs.110488	KIAA0990 protein	2.5
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.5
	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	2.5

	403356	NA	ENSP00000251525*:Hypothetical protein KI	2.5
	404983		ENSP00000252242*:Keratin, type II cytosk	2.5
	418282	AA215535	Hs.98133 ESTs	2.5
	427409	AW467143	Hs.135411 actin related protein	2.5
5	431806	AF186114	Hs.270737 tumor necrosis factor (ligand) superfam	2.5
	443367	AW071349	Hs.215937 ESTs	2.5
	421246	AW582962	Hs.102897 CGI-47 protein	2.5
	439217	AF086041	Hs.42975 ESTs	2.5
	400925		Target Exon	2.5
10	404552	NA	ENSP00000220888*:ZINC FINGER TRANSCRIPTI2.5	2.5
	417168	AL133117	Hs.81376 Homo sapiens mRNA; cDNA DKFZp586L1121 (f	2.5
	418841	NM_002332	Hs.89137 low density lipoprotein-related protein	2.5
	426853	U32974	Hs.172777 baculoviral IAP repeat-containing 4	2.5
	427738	NM_000318	Hs.180612 peroxisomal membrane protein 3 (35kD, Ze	2.5
15	457384	AA501760	Hs.15806 Homo sapiens mRNA; cDNA DKFZp434H2019 (f	2.5
	447128	AI271898	Hs.164866 cyclin K	2.5
	454893	AW813428	gb:MR3-ST0192-010200-210-c05 STD192 Homo	2.5
	434657	AA641876	Hs.191840 ESTs	2.5
	402077	NA	Target Exon	2.5
20	400289	X07820	Hs.2258 matrix metalloproteinase 10 (MMP10; str	2.5
	409723	AW885757	Hs.257862 ESTs	2.5
	447020	T27308	Hs.16986 hypothetical protein FLJ11046	2.5
	455068	AI807894	Hs.47274 Homo sapiens mRNA; cDNA DKFZp564B176 (fr	2.5
	431232	AI024353	Hs.131755 hypothetical protein FLJ14298	2.5
25	408938	AA059013	Hs.22607 ESTs	2.5
	411571	AA122393	Hs.70811 hypothetical protein FLJ20516	2.5
	426504	AW162919	Hs.170160 RAB2, member RAS oncogene family-like	2.5
	428248	AI126772	Hs.40479 ESTs	2.5
	408813	AI580090	Hs.48295 RNA helicase family	2.5
30	423504	N80077	Hs.24792 chromosome 12 open reading frame 5	2.5
	425441	AA449644	Hs.193063 Homo sapiens cDNA FLJ14201 fis, clone NT	2.5
	443066	AW297921	Hs.255703 ESTs	2.5
	443556	AA256769	Hs.94949 methylmalonyl-CoA epimerase	2.5
	428943	AW086180	Hs.37636 ESTs, Weakly similar to KIAA1392 protein	2.5
35	425320	U29344	Hs.83190 fatty acid synthase	2.5
	430388	AA356923	Hs.240770 nuclear cap binding protein subunit 2, 2	2.5
	423242	AL039402	Hs.125783 DEME-6 protein	2.5
	416241	N52639	Hs.32683 ESTs	2.5
	440244	AI743977	Hs.205144 ESTs	2.5
40	409239	AA740875	Hs.44307 ESTs, Moderately similar to I38022 hypot	2.5
	452464	AW500507	Hs.192619 KIAA1800 protein	2.5
	410718	AI920783	Hs.191435 ESTs	2.5
	408877	AA479033	Hs.130315 ESTs, Weakly similar to A47582 B-cell gr	2.5
	445150	AI446747	Hs.338704 olfactory receptor, family 7, subfamily	2.5
45	407756	AA116021	Hs.38260 ubiquitin specific protease 18	2.5
	407633	NM_007069	Hs.37189 similar to rat HREV107	2.5
	449754	H00820	Hs.30977 ESTs, Weakly similar to B34087 hypotheti	2.5
	419316	AA236255	Hs.298419 ESTs	2.5
	429118	H20869	Hs.36406 ESTs, Highly similar to unnamed protein	2.5
50	440331	AL046412	Hs.202151 ESTs	2.5
	449344	AI640355	Hs.312691 ESTs	2.5
	459006	AW298631	Hs.27721 Wolf-Hirschhorn syndrome candidate 1-lik	2.5
	423165	AI937547	Hs.124915 hypothetical protein MGC2601	2.5
	411337	AW837349	gb:QV2-LT0038-270300-108-d12 LT0038 Homo	2.5
55	438290	AA843719	Hs.122341 ESTs	2.5
	406414		C5000506*gl 124941 sp P18614 ITA1_RAT I	2.5
	424498	AB033043	Hs.149377 hypothetical protein DKFZp761L0424	2.5
	443464	BE548446	Hs.5167 Homo sapiens mRNA; cDNA DKFZp434F152 (fr	2.5
	424856	AA347746	Hs.9521 ESTs, Weakly similar to ZN43_HUMAN ZINC	2.5
60	440304	BE159984	Hs.125395 ESTs	2.5
	409045	AA636062	Hs.50094 Homo sapiens mRNA; cDNA DKFZp434O0515 (f2.5	2.5
	422648	D86983	Hs.118893 Melanoma associated gene	2.5
	428819	AL135623	Hs.193914 KIAA0575 gene product	2.5
	412520	AA442324	Hs.795 H2A histone family, member O	2.5
65	430802	D13752	Hs.184927 cytochrome P450, subfamily XIB (steroid	2.5
	408031	AA081395	Hs.42173 Homo sapiens cDNA FLJ10366 fis, clone NT	2.5
	403133		Target Exon	2.5

413189	BE070231	gb:QV4-BT0407-260100-087-f12 BT0407 Homo	2.5
400346	AB041269	Hs.272263 Homo sapiens mRNA for keratin 19, partial	2.5
435509	AI458679	Hs.181915 ESTs	2.5
458145	AI239457	Hs.130794 ESTs	2.5

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TABLE 19A

Table 19A shows the accession numbers for those pkeys lacking unigeneID's for Table 19. For each probeset, we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
407647	1007366_1	AW860158 AW862385 AW860159 AW862386 AW862341 AW821869 AW821893 AW062660 AW062656
407980	103087_1	AAC46309 AI263500 AAO46397
408254	1049346_1	AW807227 AW807576 AW807137 AW807157 AW807495 AW807494 AW807417 AW807083 AW845786 AW845801 AW807130 AW807335 AW807081 AW807349 AW807339 AW807164 AW807341 AW807224 AW845903 AW177424 AW807159 AW807123 BE141576 AW807340 AW807334 AW807520 AW807205 AW807505 BE141574 AW807390 AW807395 AW845789 AW807101 AW807089 AW807519 AW807239 AW807509 AW807356 AW807525 AW807098 AW807307 AW807153 AW807295 AW807313 AW807322 AW807265 AW807513 AW807516 AW807166 AW807501 AW807120 AW807168 AW807121 AW807527 AW807151 AW807203 AW807489 AW807511 AW807158 AW845800 AW807507 AW845793 AW845796 AW807296 AW845781 AW807444 AW845871 AW807512 AW807242 AW807141 AW807522 AW807487 AW807514 AW807142 AW807232 AW807379 AW807114 AW807518 AW807199 AW807211 AW807498 AW807086 AW807492 AW807218 AW807082 AW807525 AW807493 AW807523 AW807087 AW845784 AW807037 AW807128 AW807080 AW807118 AW845807 AW807524 AW845803 AW807249 AW845795 AW807160 AW807343 AW807515 AW807233 AW807289 AW177102 AW807352 AW807394 AW177105 AW807176 AW177103 AW845870 AW177099 AW177101 AW807528 AW807336 AW807038 AW177100 AW807411 AW807088 AW845865 AW807226 AW807517 AW807397 AW807303 AW807177 AW807154 AW807136 AW807146 AW807085 AW807521 AW807488 AW807385 AW807355 AW807223 AW807155
409163	110418_1	AA065081 AA075017 AA084791 AA071015 AA081560 AA071459 AA545727 AA083100 AA085356 AA115845 AA075457 AA064704 AA082878 AA075742 AA069162
409695	114876_1	AA266961 AA296889 AA076945 AA077528 AA077497
410534	1207247_1	AW905138 AW753008 R13818 Z43519
410672	1214882_1	AW794600 AW794730
410784	1221005_1	AW803201 BE079700 BE062940
410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803258 AW803396 AW803334 AW803355
410835	1223785_1	AW806906 AW806915 AW865460 AW866475 AW866462 AW866448 AW866372 AW866604
411050	1230330_1	AW814902 BE156556 BE156867 BE156590 BE156441 BE156447
411086	1231500_1	BE070800 AW875226 BE149115
411093	1231970_1	BE067650 AW817053
411111	1232669_1	AW818127 AW818161 R09719
411171	1234393_1	AW820260 AW820332 R94406
411337	1239217_1	AW837349 AW837355 AW882717
411514	1248638_1	AW850178 AW850233 AW850445 AW850446
411670	1253680_1	AW856552 AW861101 AW856574 AW861099 AW861100 AW856573 AW856576 AW856562
411905	1265181_1	BE265067 BE264978 AW875420
412102	1277395_1	H56435 H56572 AW892929
412209	1283610_1	AW901456 AW901450 AW901441
412248	1285000_1	BE176480 AW803298 AW903313
413043	1346553_1	BE158766 BE061699 BE147362 BE061666 BE061697 BE061647 BE061678
413111	1349546_1	BE065837 BE065805 BE065799 BE065818 BE065839 BE065831 BE065894 BE065789 BE065792
413189	1352723_1	BE070231 BE070229 BE070255
413221	1353887_1	BE161151 BE162495 BE161002 BE072205 BE160989 BE162482
413499	1373910_1	BE144884 H97942
413708	1384140_1	BE158791 BE158806 BE158748 BE158744 BE158740 BE158739 BE158811 BE158700 BE158741 BE158683 BE158685
414210	1426051_1	BE383592 BE261671
414596	1465004_1	BE386870 Z41986 H08501